
MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Fri Oct 1 13:52:39 1999; MasPar time 25.13 Seconds
 Tabular output not generated.
 Title: >US-09-026-400-2
 Description: (1-461) from US09026400.pap
 Perfect Score: 3223
 Sequence: 1 MVHQSHGHGEAAAAANGKS.....LERVKFCQRNKKNSINGC 461

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Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29 30:part30 31:part31 32:part32 33:part33
 34:part34 35:part35 36:part36 37:part37 38:part38
 39:part39

Statistics: Mean 35.539; Variance 164.075; scale 0.217

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	3223	100.0	461	34	Nicotianamine aminotr	4.56e-283
2	2888	89.6	551	34	Nicotianamine aminotr	7.13e-252
3	403	12.5	394	26	Aquifex aspartate ami	8.25e-24
4	277	8.6	373	26	Aquifex aspartate ami	4.95e-13
5	276	8.6	398	26	Ammonifex degensii as	6.00e-13
6	231	7.2	482	26	Barley alanine aminot	3.19e-09
7	222	6.9	517	20	Carnation ACC synthas	1.73e-08
8	216	6.7	422	17	Human kynurenine amin	5.30e-08
9	209	6.5	423	17	Rat kynurenine aminot	1.95e-07
10	209	6.5	437	17	Rat kynurenine aminot	1.95e-07
11	209	6.5	457	17	Rat kynurenine aminot	1.95e-07
12	195	6.1	496	7	Rat ALR.	2.57e-06
13	180	5.6	480	32	Rose 1-aminocycloprop	3.93e-05
14	179	5.6	493	5	ACC synthetase.	4.71e-05
15	178	5.5	486	23	Poplar 1-aminocyclopr	5.64e-05
16	178	5.5	493	3	Zucchini ACC synthase	5.64e-05

17	178	5.5	493	29	W47311	Zucchini ACC synthase	5.64e-05
18	177	5.5	493	29	W47310	Protein encoded by zu	6.75e-05
19	177	5.5	493	3	R15504	Zucchini ACC synthase	6.75e-05
20	176	5.5	496	30	W46904	A human mutant alanin	8.08e-05
21	176	5.5	496	34	W62267	Modified human alanin	8.08e-05
22	175	5.4	493	7	R35230	Human ALR.	9.66e-05
23	169	5.2	362	20	W04559	Carnation ACC synthas	2.83e-04
24	166	5.2	494	29	W47312	Zucchini ACC synthase	4.82e-04
25	166	5.2	494	3	R15863	Zucchini ACC synthase	4.82e-04
26	165	5.1	469	3	R15510	Tomato ACC synthase e	5.75e-04
27	157	4.9	323	29	W37444	1-aminocyclopropane-1	2.36e-03
28	155	4.8	359	14	R72715	hisc gene product of	3.35e-03
29	148	4.6	363	26	W24256	Ammonifex histidinol-	1.13e-02
30	145	4.5	481	23	W21754	Poplar 1-aminocyclopr	1.90e-02
31	146	4.5	482	32	W60233	Pelargonium 1-aminocy	1.60e-02
32	146	4.5	482	32	W60234	Pelargonium 1-aminocy	1.60e-02
33	138	4.3	496	10	R53114	Crucifer 1-aminocyclo	6.29e-02
34	136	4.2	414	26	W24248	Aquifex aspartate tra	8.83e-02
35	135	4.2	485	3	R15507	Tomato ACC synthase e	1.05e-01
36	135	4.2	485	28	W39422	ACC synthase protein.	1.05e-01
37	135	4.2	485	29	W47314	Tomato ACC synthase L	1.05e-01
38	134	4.2	487	31	W57484	Papaya ACC synthase e	1.24e-01
39	133	4.1	390	22	W09879	ACC synthase GAC-2.	1.46e-01
40	133	4.1	485	3	R15506	Tomato ACC synthase e	1.46e-01
41	133	4.1	485	29	W47313	Tomato ACC synthase.	1.46e-01
42	125	3.9	330	19	R98599	Broccoli ACC synthase	5.56e-01
43	127	3.9	333	3	R13494	P.denitrificans COB C	3.99e-01
44	125	3.9	374	19	R98598	Broccoli ACC synthase	5.56e-01
45	125	3.9	490	32	W60235	Pelargonium 1-aminocy	5.56e-01

ALIGNMENTS

RESULT 1
 ID W61642 standard; Protein; 461 AA.
 AC W61642;
 DT 27-OCT-1998 (first entry)
 DE Nicotianamine aminotransferase 49564.15 molecular weight protein.
 KW nicotianamine aminotransferase; plant; iron absorption;
 OS iron deficiency chlorosis.
 FN Gramineae sp.
 PN EP-860499-A2.
 PD 26-AUG-1998.
 PF 19-FEB-1998; 102891.
 PR 21-FEB-1997; JP-037499.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 PI Mori S; Nakanishi H; Takahashi M;
 DR WPI; 98-439341/38.
 DR N-PSDB; W48147.
 PT New nicotianamine aminotransferase protein and DNA - useful for
 enhancing iron absorption of plant cells
 PS Claim 3; page 12-13; 17pp; English.
 CC The nicotianamine aminotransferase can be used in a plasmid to transform
 plant cells to produce cells with enhanced iron absorption, and it is
 implied [though not stated] that plants with improved resistance to iron
 deficiency chlorosis in calcareous soils can be regenerated from the
 transformed cells. The gene fragment can be used to detect, amplify
 CC and/or isolate nicotianamine aminotransferase genes.
 SQ Sequence 461 AA;

Query Match 100.0%; Score 3223; DB 34; Length 461;
 Best Local Similarity 100.0%; Pred. No. 4.56e-283;
 Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 mvhqsngheaaaaaangksnghaaaangksnghaaaavewnfargkdglattgaks 60
 |||||||

QY 1 MVHQSHGHGEAAAAANGKSNGHAAAAANGKSNGHAAAAVFNFAFGKDGILLATTGAKNS 60
 |||||||

Db 61 iralrykisavveesgrrpvlplahqpsvfpafitaveaedavaaalrtgqfncyaav 120
 |||||||

QY 61 IRAIRYKISAVVEESGRRPVLPLAHGDPVFPFRTAVEAEDAVAAALRTGQFNCYAGV 120
 |||||||

Db 121 glpaarsavaehlsqgvyklsaddvfltaggtqaleviplaqtaganillprpgypn 180

QY 121 GLPAARSAVAEHLGSGVYKLSADDDVLTAGTQAEVLIIPVLAQTAGANILLPRGYPN 180
 Db 181 yearaafnklevrfdllpdkgwedidslesiadknttamvlpnnpccsvsydhla 240
 QY 181 YEARAFAFNKLEVRHFDLIPDKGWEIDIDSLESIAADKNTAMVLIIPNPNPCGSVSYDHIA 240
 Db 241 kvaevarklgilviadevygkvlgsapfipmgvfgghiapvlsglskskswilpqrwg 300
 QY 241 KVAEAVARKLGILVIADEVYKVLGSLGAPFIPMGVFGGHIAVPLVSLGSLKSWILPQWRG 300
 Db 301 vavydptkilektkistsitnlnvstddpatfvqalpkilntkadvfkfrkiigllkess 360
 QY 301 VAVYDPTKILEKTKISTITNVLNVDTPATFVQALPKILENTKADFKFRKIIGLLKESS 360
 Db 361 eicyreikenkyitophkpegsmfvmvknlnllleehddidfccklakeesvilpcpsv 420
 QY 361 EICYREIKENKYITCPHKPEGSMFVMVKNLNLHLEIEHDDIDFCCKLAKEESVILPCPSV 420
 Db 421 lmenwvritfacvpslqdglerkysfcgrnkknsgnc 461
 QY 421 LGMENWVRITFACVPSLQDGLERVKSCQRNKKNSINGC 461

RESULT 2
 ID W61643 standard; Protein; 551 AA.
 AC W61643;
 DT 27-OCT-1998 (first entry)
 DE Nicotianamine aminotransferase 58148.62 molecular weight protein.
 KW Nicotianamine aminotransferase; plant; iron absorption;
 OS Gramineae sp.
 PN EP-860499-A2.
 PD 26-AUG-1998.
 PF 19-FEB-1998; 102891.
 PR 21-FEB-1997; JP-037499.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 PI Mori S, Nakanishi H, Takahashi M;
 DR WPI: 98-439341/38.
 DR N-PSDB; V48148.
 PT New nicotianamine aminotransferase protein and DNA - useful for
 enhancing iron absorption of plant cells
 PS Claim 3; Page 14-15; 17pp; English.
 CC The nicotianamine aminotransferase can be used in a plasmid to transform
 plant cells to produce cells with enhanced iron absorption, and it is
 implied [though not stated] that plants with improved resistance to iron
 deficiency chlorosis in calcareous soils can be regenerated from the
 CC transformed cells. The gene fragment can be used to detect, amplify
 CC and/or isolate nicotianamine aminotransferase genes.
 SQ Sequence 551 AA;

Query Match 89.6%; Score 2888; DB 34; Length 551;
 Best Local Similarity 88.1%; Pred. No. 7.13e-252;
 Matches 409; Conservative 30; Mismatches 20; Indels 5; Gaps 1;
 Db 88 resnghaeaaadngesnehaedaaesngshaaaaaevevfnagdkdvglaatga 147
 QY 3 HQSNGHGEAAAAAANGKSNHAAAAANGKSNHAAAAA-----VEWNFARGKDGILATGA 57
 Db 148 nmsirairyikisavqekgrprvplahgdpvfpafirtaveadaavaavrtggfncyp 207
 QY 58 KNSIRAIRYIKISAVESGSRPVLPALHGDPSVFPFARTAVEADAVALAARTGQFNCA 117
 Db 208 agvlparsavaehlsqgypymlsaddvftagdtgaievlpvtaqtaganillprpg 267
 QY 118 AGVLPARSAVAEHLGSGVYKLSADDDVLTAGTQAEVLIIPVLAQTAGANILLPRPG 177
 Db 268 ypnyearaafnrlvrhfdllpdkgwedidslesiadknttamvlpnnpccsvsydh 327
 QY 178 YPNYEAFAFNKLEVRHFDLIPDKGWEIDIDSLESIAADKNTAMVLIIPNPNPCGSVSYD 237
 Db 328 hlskvaevarklgilviadevygkvlgsapfipmgvfgghiapvlsglskskswilpqrwg 387

QY 238 HLAKVAEAVARKLGILVIADEVYKVLGSLGAPFIPMGVFGGHIAVPLVSLGSLKSWILPQWR 297
 Db 388 lgvavvdyprkilcetkistsitnlnvstddpatfvqalpkilntkadvfkfrkiigllk 447
 QY 298 LGWAVVDPYKILSEKTKISTITNVLNVDTPATFVQALPKILENTKADFKFRKIIGLLK 357
 Db 448 esselcykqikenkyitophkpegsmfvmvknlnllleehddidfccklakeesvilcp 507
 QY 358 ESSEICYREIKENKYITCPHKPEGSMFVMVKNLNLHLEIEHDDIDFCCKLAKEESVILCP 417
 Db 508 gsvlgmanwvritfacvpslqdglerkysfcgrnkknsgnc 551
 QY 418 GSVILGMENWVRITFACVPSLQDGLERVKSCQRNKKNSINGC 461

RESULT 3
 ID W24257 standard; Protein; 394 AA.
 AC W24257;
 DT 18-FEB-1998 (first entry)
 DE Aquifex aspartate aminotransferase VF5/AA.
 KW Aspartate aminotransferase; VF5/AA; chiral compound.
 OS Aquifex sp. strain VF5.
 PN W09729187-A1.
 PD 14-AUG-1997.
 PF 21-JAN-1997; U01094.
 PR 08-MAY-1996; US-646590.
 PR 09-FEB-1996; US-599171.
 PA (RECO-) RECOMBINANT BIOCATALYSIS INC.
 PI Swanson RV, Warren PV;
 DR WPI: 97-415343/38.
 DR N-PSDB; T78781.
 PT New transaminase(s) and aminotransferase(s) derived from host cells
 PT - used for producing enzymes, and hybridisation probes for a cDNA or
 genomic library
 PS Claim 19; Fig 10; 95pp; English.
 CC This protein sequence comprises aspartate aminotransferase VF5/AA
 of Aquifex VF5, a strictly chemolithoautotrophic marine eubacterium
 CC which grows optimally at 85-90 deg C and pH 6.8 in high salt
 CC medium. The VF5/AA amino acid sequence was deduced from genomic
 CC DNA (see J78781). Claimed thermostable transaminases and
 CC aminotransferases (W24248-57) can be produced from native or
 CC recombinant host cells for use with L- and/or D-amino acids for
 CC production of optically pure chiral compounds used in the
 CC pharmaceutical, agricultural and other industries. A method is
 CC claimed for transferring an amino group from an amino acid to an
 CC alpha-keto acid using a claimed enzyme. The measurement of
 CC aspartate aminotransferase levels in blood serum is used as an
 CC indicator of heart damage.
 SQ Sequence 394 AA;

Query Match 12.5%; Score 403; DB 26; Length 394;
 Best Local Similarity 29.1%; Pred. No. 8.25e-24;
 Matches 106; Conservative 87; Mismatches 145; Indels 26; Gaps 25;
 Db 42 pdfdtpdfikeaciralregtkk-vapsagibelreaieakllkenkveyk-pleiv-vs 98
 QY 92 PAPRTAVEADEAAVALRTGQFNCHYAGVGLGPAARSAVAEHL-SQG-VPYKLSADDDVLT 149
 Db 99 agakmvlifmailde--gdevllpspywtytpeqirffgvgpv-evplkkekfgqlsl 155
 QY 150 AGGTQAI-EVLIIPVLAQTAGANILLPRPGYPNYEARAAAF-NKLEVRHFDLIPDKGWEIDI 207
 Db 156 edvkekvtter-tkaivinspnptgavveeeekkkiaefcverqifiidecyeyfyvgd 214
 QY 208 DSL-ESIAADKNTAMVLIIPNPNPCGSVSYDHLAKVAEAVARKLGILVIADEVYKVLGSL 266
 Db 215 akvfspasfdevknitftvnafsksysmtgwigva-c-peey-akv-ia-slns-qs 268
 QY 267 APFIPMGVFGH-TAPV-LSIGSLKSWILPQWRGAVVYDPTKILEKTKISTITNVLN 324
 Db 269 vs-nvttfagqyal-ealnpkpskdfvnmnaferrrtaveelskipgmdiv-kpega 325
 QY 325 VSTDPTATFVQ-EALPKILENTKA-DEFFKRIIGLLKESSEICYREIKENKYITCPHKPEGS 382

CC consequences associated with the aging processes in the brain.
 CC This is the human KAT sequence. Three rat KAT clones are described
 CC in T11560, T11742-43.
 SQ Sequence 422 AA;

Query Match 6.7%; Score 216; DB 17; Length 422;
 Best Local Similarity 30.6%; Pred. No. 5.30e-08;
 Matches 34; Conservative 29; Mismatches 47; Indels 1; Gaps 1;
 Db 149 igtngelssnwgldpmlagktsrtkalvlnpnpnlgkfvksreelvaslcqghdv 208
 QY 192 VRHFDLIPDKGWEIDDSLESDAKNTTAMVIINPNPCGSVSYDHLAKVAEVRKLG 251
 Db 209 voitdevygmvydghqhisiaslpgmwtltsagktsfsgtgvkv 259
 QY 252 LVIADDEVYKLVGSAPFIPMGVFGHI-APVLSIGLSKSWIVPGWRLGW 301

RESULT 9
 ID R89896 standard; Protein; 423 AA.
 AC R89896;
 DT 14-JUL-1996 (first entry)
 DE Rat kynurenine aminotransferase (KAT) clone.
 KW Kynurenine aminotransferase; KAT; kynurenine acid; KYNA; kynurenine;
 KW KYN; brain; NMDA receptor; glutamatergic function.
 OS Rattus rattus.
 PN WO9601893-Al.
 PD 25-JAN-1996.
 PR 23-JUN-1995; U07855.
 PR 07-JUL-1994; US-271667.
 PA (PHAA) PHARMACIA SPA.
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 PI Benatti L, Breton J, Mosca M, Okuno E, Schwarcz R;
 PI Speciale C;
 DR WPI; 96-097623/10.
 DR N-PSDB; T11560.
 PT Isolated DNA encoding mammalian kynurenine amino:transferase (KAT) -
 PT useful in gene therapy applications and for identifying KAT in brain
 PT tissue
 PS Claim 16; Figure 2; 5lpp; English.
 CC Sequences encoding Kynurenine aminotransferase (KAT) can be inserted
 CC into vectors and subsequently cells and hence can be used for gene
 CC therapy. The vector and host cells can be used for cerebral
 CC implantation to where KAT can directly catalyze the production of
 CC kynurenic acid (KYNA) from kynurenine (KYN). It is thought KYNA acts
 CC as a negative endogenous modulator of cerebral glutamatergic
 CC function. KYNA concentrations and the activity of KAT show an
 CC increase with age. KAT inhibitors, by providing an increase of the
 CC glutamatergic tone at the NMDA receptor, could be useful in
 CC situations where NMDA receptor function is insufficient and/or KAT
 CC activity and KYNA levels are abnormally enhanced. Hence they could
 CC be particularly useful in the treatment of the pathological
 CC consequences associated with the aging processes in the brain.
 CC Three KAT clones are described in T11560, T11742-43.
 SQ Sequence 423 AA;

Query Match 6.5%; Score 209; DB 17; Length 423;
 Best Local Similarity 33.0%; Pred. No. 1.95e-07;
 Matches 35; Conservative 24; Mismatches 46; Indels 1; Gaps 1;
 Db 154 lgasndwldpaelaskftprtkvlnpnpnlgkfvksrmelelvancqghdvvcisd 213
 QY 197 LIPDKGWEIDDSLESDAKNTTAMVIINPNPCGSVSYDHLAKVAEVRKLG 256
 Db 214 evyqvlvdyghqhsiaslpgmwdrtltsagktsfsgtgvkv 259
 QY 257 EYVYKLVGSAPFIPMGVFGHI-APVLSIGLSKSWIVPGWRLGW 301

RESULT 10
 ID R89897 standard; Protein; 437 AA.
 AC R89897;
 DT 14-JUL-1996 (first entry)

DE Rat kynurenine aminotransferase (KAT) clone.
 KW Kynurenine aminotransferase; KAT; kynurenine acid; KYNA; kynurenine;
 KW KYN; brain; NMDA receptor; glutamatergic function.
 OS Rattus rattus.
 PN WO9601893-Al.
 PD 25-JAN-1996.
 PR 23-JUN-1995; U07855.
 PR 07-JUL-1994; US-271667.
 PA (PHAA) PHARMACIA SPA.
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 PI Benatti L, Breton J, Mosca M, Okuno E, Schwarcz R;
 PI Speciale C;
 DR WPI; 96-097623/10.
 DR N-PSDB; T11742.
 PT Isolated DNA encoding mammalian kynurenine amino:transferase (KAT) -
 PT useful in gene therapy applications and for identifying KAT in brain
 PT tissue
 PS Claim 16; Figure 3; 5lpp; English.
 CC Sequences encoding Kynurenine aminotransferase (KAT) can be inserted
 CC into vectors and subsequently cells and hence can be used for gene
 CC therapy. The vector and host cells can be used for cerebral
 CC implantation to where KAT can directly catalyze the production of
 CC kynurenic acid (KYNA) from kynurenine (KYN). It is thought KYNA acts
 CC as a negative endogenous modulator of cerebral glutamatergic
 CC function. KYNA concentrations and the activity of KAT show an
 CC increase with age. KAT inhibitors, by providing an increase of the
 CC glutamatergic tone at the NMDA receptor, could be useful in
 CC situations where NMDA receptor function is insufficient and/or KAT
 CC activity and KYNA levels are abnormally enhanced. Hence they could
 CC be particularly useful in the treatment of the pathological
 CC consequences associated with the aging processes in the brain.
 CC Three KAT clones are described in T11560, T11742-43.
 SQ Sequence 437 AA;

Query Match 6.5%; Score 209; DB 17; Length 437;
 Best Local Similarity 33.0%; Pred. No. 1.95e-07;
 Matches 35; Conservative 24; Mismatches 46; Indels 1; Gaps 1;
 Db 168 lgasndwldpaelaskftprtkvlnpnpnlgkfvksrmelelvancqghdvvcisd 227
 QY 197 LIPDKGWEIDDSLESDAKNTTAMVIINPNPCGSVSYDHLAKVAEVRKLG 256
 Db 228 evyqvlvdyghqhsiaslpgmwdrtltsagktsfsgtgvkv 273
 QY 257 EYVYKLVGSAPFIPMGVFGHI-APVLSIGLSKSWIVPGWRLGW 301

RESULT 11
 ID R89898 standard; Protein; 457 AA.
 AC R89898;
 DT 14-JUL-1996 (first entry)
 DE Rat kynurenine aminotransferase (KAT) clone.
 KW Kynurenine aminotransferase; KAT; kynurenine acid; KYNA; kynurenine;
 KW KYN; brain; NMDA receptor; glutamatergic function.
 OS Rattus rattus.
 PN WO9601893-Al.
 PD 25-JAN-1996.
 PR 23-JUN-1995; U07855.
 PR 07-JUL-1994; US-271667.
 PA (PHAA) PHARMACIA SPA.
 PA (UYMA-) UNIV MARYLAND BALTIMORE.
 PI Benatti L, Breton J, Mosca M, Okuno E, Schwarcz R;
 PI Speciale C;
 DR WPI; 96-097623/10.
 DR N-PSDB; T11743.
 PT Isolated DNA encoding mammalian kynurenine amino:transferase (KAT) -
 PT useful in gene therapy applications and for identifying KAT in brain
 PT tissue

PS Claim 16; Figure 4; 5lpp; English.
 CC Sequences encoding Kynurenine aminotransferase (KAT) can be inserted
 CC into vectors and subsequently cells and hence can be used for gene
 CC therapy. The vector and host cells can be used for cerebral
 CC implantation to where KAT can directly catalyze the production of

CC kynurenic acid (KYNA) from kynurenine (KYN). It is thought KYNA acts
 CC as a negative endogenous modulator of cerebral glutamatergic
 CC function. KYNA concentrations and the activity of KAT show an
 CC increase with age. KAT inhibitors, by providing an increase of the
 CC glutamatergic tone at the NMDA receptor, could be useful in
 CC situations where NMDA receptor function is insufficient and/or KAT
 CC activity and KYNA levels are abnormally enhanced. Hence they could
 CC be particularly useful in the treatment of the pathological
 CC consequences associated with the aging processes in the brain.
 CC Three KAT clones are described in T11560, T11742-43.
 CC Sequence 457 AA;
 SQ

Query Match 6.5%; Score 209; DB 17; Length 457;
 Best Local Similarity 33.0%; Pred. No. 1.95e-07;
 Matches 35; Conservative 24; Mismatches 46; Indels 1; Gaps 1;
 188 lqasndwldpaelskftprtkvlnvntnnpplgkvfsmelavlncqhdvvcisd 247
 QY 197 LIPDKGWEIDIDSLESIAKNTTAMVIINPNPNCVSYSDHLAKYAEVARKLGILVIAD 256
 Db 248 evyqvlvydghvhsiaslpgmwdtrlttigsagksfsatgkwgvwv 293
 QY 257 EYVKLVGSAPFPMGVFCHI-APVLSIGSLKSWIVPCWGLGWV 301

RESULT 12
 ID R35231 standard; Protein; 496 AA.
 AC R35231;
 DT 10-AUG-1993 (first entry)
 DE Rat ALT.
 KW Primer; polymerase chain reaction; PCR; amplify; human; diagnosis;
 KW alanine aminotransferase; ALT; marker; hepatic disease; serum.
 OS Rattus rattus.
 PN J05068548-A.
 PD 23-MAR-1993.
 PF 06-AUG-1991; 222318.
 PR 06-AUG-1991; JP-222318.
 PA (KAGA) KAGAKU OYOBI KESSEI RYOHO KENKYUSHO.
 DR WPI: 93-136892/17.
 DR N-PSDB: Q35231.
 PT Human alanine-amino-transferase gene fragments - used as marker
 PT in diagnosing hepatic diseases
 PS Disclosure; Page 11-13; 15pp; Japanese.
 CC The sequences given in R35230-31 represent human and rat alanine
 CC aminotransferase (ALT) genes respectively. ALT is an important
 CC marker in the diagnosis of hepatic disease. Gene fragments of ALT
 CC can be used in inexpensive, large scale production of human ALT
 CC which can then be used as a standard in the determination of human
 CC serum ALT. See also Q40500-01.
 CC Sequence 496 AA;
 SQ

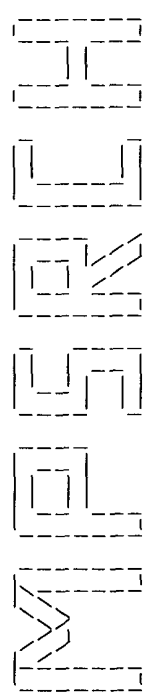
Query Match 6.1%; Score 195; DB 7; Length 496;
 Best Local Similarity 29.2%; Pred. No. 2.57e-06;
 Matches 45; Conservative 42; Mismatches 56; Indels 11; Gaps 9;
 123 ysissgipredvacyierddgipadpnniflstgasdaivtmklivsggeartgv 182
 QY 116 YRAGVGLPAARSAVAEHLISQ-GVPYKLSADDVFLTAGGTQAEIIVPLAQTAG-A-NI 171
 Db 183 ltipyplysaaladavqdyv-ldeeravaldiaelrralcalqardccprvlecin 241
 QY 172 LLPRPGYPNYEAR-AAFNKLEVRHFDPKGEWIDIDSLE-SI--A-DKN-TTANVIIN 225
 Db 242 pgnptqvqtrecieavirfafkegflmdevy 275
 QY 226 PNNPCSVSYSDHLAKYAEVARKLGILVIADDEVY 259

RESULT 13
 ID W60239 standard; Protein; 480 AA.
 AC W60239;
 DT 28-SEP-1998 (first entry)
 DE Rose 1-aminocyclopropane-1-carboxylase synthase.

KW ACC synthase; 1-aminocyclopropane-1-carboxylate synthase;
 KW ethylene; transgenic plant; wilting; rose; pRosekacc7.
 OS Rosa sp. cv. Red Cardinal.
 PN W09814465-AL.
 PD 09-APR-1998.
 PF 30-SEP-1997; U17644.
 PR 01-OCT-1996; US-724194.
 PA (COLS) UNIV COLORADO STATE RES FOUND.
 PI Ranu RS;
 DR WPI: 98-260994/23.
 DR N-PSDB: V30330.
 PT New isolated ACC synthase genes - are obtained from geranium and
 PT rose, used to develop products for producing plants with reduced
 PT ethylene levels, for increasing shelf-life
 PS Claim 60; Fig 10; 77pp; English.
 CC This amino acid sequence of this 1-aminocyclopropane-1-carboxylate
 CC synthase (ACC synthase) of rose cv. Red Cardinal was deduced from
 CC isolated cDNA clone prosekacc7 (see V30330). The invention relates
 CC to new isolated ACC synthase genes from geranium and rose (see
 CC V30324-26 and V30330) and the use of antisense fragments of these
 CC genes to control expression of ACC synthase genes in transgenic
 CC plants, especially in geranium, rose and woody plants. By reducing
 CC the amount of ACC synthase produced in plant cells, the rate of ACC
 CC conversion to ethylene can be decreased. This can be used to
 CC prolong the shelf-life of cut flowers and to reduce leaf yellowing
 CC and petal abscission during shipping and storage.
 CC Sequence 480 AA;
 SQ

Query Match 5.6%; Score 180; DB 32; Length 480;
 Best Local Similarity 27.0%; Pred. No. 3.93e-05;
 Matches 48; Conservative 50; Mismatches 70; Indels 10; Gaps 7;
 120 geelgisgiacyqpsdglmelklavagfmskaignsvtynpqsvlttagatpaieilsfc 179
 QY 105 AALETGQFNCTAGAGVGLPAARSAVAEHLISQGVPKLS--ADDVFLTAGGTQAEIIVPV 162
 Db 180 lads-gnaflpapyppgldrdvkwrtgveilpypcrsadtfnlsitaldrafnqakrg 238
 QY 163 LAQTAGANILLPRPGYPNYEARAFNK-LEVRHFDPKGEWIDIDSLE-SIAD-KNTT 219
 Db 239 vkvrgiisnpsnpgsgslltreslynlldfareknhhiisnelfagstyggseefvma 296
 QY 220 AMV---II-NPNPCSVSYSDHLAKYAEVARKLGILVIADDEVYKLVGSAPFIPMG 273

RESULT 14
 ID R25406 standard; Protein; 493 AA.
 AC R25406;
 DT 18-JAN-1993 (first entry)
 DE ACC synthetase.
 KW 1-aminocyclopropane-1-carboxylic acid synthetase; detriment;
 KW ethylene; growth; maturity; aging; plant.
 OS Cucurbita maxima.
 PN J04169183-A.
 PD 17-JUN-1992.
 PR 31-OCT-1990; 296943.
 PR 31-OCT-1990; JP-296943.
 PA (SUMO) SUMITOMO CHEM CO LTD.
 DR WPI: 92-253389/31.
 DR N-PSDB: Q25896.
 PT Detriment induced ACC synthetase gene - used for control of
 PT bio-synthesis of ethylene, for controlling growth, maturity and
 PT ageing of higher plant
 PS Claim 2; Fig 1; 10pp; Japanese.
 CC The protein sequence was deduced from the DNA sequence of the gene
 CC encoding detriment induced 1-aminocyclopropane-1-carboxylic acid
 CC (ACC) synthetase (EC 4.4.1.14) which was obtcd. by screening a cDNA
 CC library prepd. from Cucurbita maxima mRNA. EC4.4.1.14 obtcd. from
 CC cDNA library clones was screened by an antibody method to identify
 CC colonies producing EC 4.4.1.14, e.g. E.coli DH5 alpha/PCMW33.
 CC Biosynthesis of ethylene is controlled by ACC synthetase. Ethylene
 CC controls the growth, maturing and aging of higher plants.
 CC Sequence 493 AA;
 SQ



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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Oct 1 13:50:56 1999; Waspar time 33.04 Seconds
761.473 Million cell updates/sec
Tabular output not generated.

Title: >US-09-026-400-2
Description: (1-461) from US09026400.pep
Perfect Score: 3223
Sequence: 1 MVHQSGHGAAAAANGKS.....LVRVKFCQKNKKNSINGC 461

Scoring table: PAM 150
Gap 11

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: sptrembl9
1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phase 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 49.304; Variance 91.106; scale 0.541

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	1275	39.6	389	10	049451 TYROSINE TRANSAMINASE- F42D1.2 PROTEIN	2.31e-248
2	726	22.5	464	5	093703 ASPARTATE AMINOTRANSFERASE	1.33e-125
3	495	15.4	429	2	033267 PUTATIVE AMINOTRANSFERASE	1.44e-75
4	460	14.3	401	2	086587 PUTATIVE AMINOTRANSFERASE	3.71e-68
5	439	13.6	401	1	059044 401AA LONG HYPOTHETICAL	9.70e-64
6	435	13.5	404	2	F71348 ASPARTATE AMINOTRANSFERASE	6.69e-63
7	410	12.7	405	2	P77727 FROM BASES 2401667 TO 1.11e-57	1.11e-57
8	403	12.5	394	2	067781 ASPARTATE AMINOTRANSFERASE	3.15e-56
9	401	12.4	402	2	088124 PUTATIVE AMINOTRANSFERASE	8.18e-56
10	374	11.6	390	2	025383 SOLUTE-BINDING SIGNATURE	3.08e-50
11	368	11.4	357	2	005237 HYPOTHETICAL 39.5 KD P	5.20e-49
12	365	11.3	397	2	060013 ASPARTATE AMINOTRANSFERASE	2.14e-48
13	361	11.2	397	2	053870 PUTATIVE AMINOTRANSFERASE	1.41e-47
14	342	10.6	382	2	054170 391AA LONG HYPOTHETICAL	1.03e-43
15	330	10.2	391	1	058489 ASPARTATE AMINOTRANSFERASE	7.75e-41
16	323	10.0	379	1	028151 ASPARTATE AMINOTRANSFERASE	7.02e-40
17	299	9.3	389	1	059036 389AA LONG HYPOTHETICAL	4.29e-35
18	296	9.2	383	1	033822 ASPARTATE AMINOTRANSFERASE	1.68e-34
19	295	9.2	385	2	056232 ASPARTATE AMINOTRANSFERASE	2.65e-34
20	294	9.1	374	1	027916 ASPARTATE AMINOTRANSFERASE	4.17e-34

21	290	9.0	390	1	038650 ASPARTATE AMINOTRANSFERASE	2.56e-33
22	283	8.8	400	2	086459 PUTATIVE ASPARTATE AMINOTRANSFERASE (ASPC)	6.08e-32
23	277	8.6	373	2	066737 AMINOTRANSFERASE (ASPC)	9.05e-31
24	268	8.3	432	1	Q58874 HYPOTHETICAL PROTEIN M	5.09e-29
25	263	8.2	389	2	Q55128 HYPOTHETICAL AMINOTRANSFERASE	4.71e-28
26	261	8.1	418	5	Q21658 R03A10.4 PROTEIN.	1.15e-27
27	259	8.0	371	2	053091 ORF.	2.78e-27
28	256	7.9	152	10	049450 HYPOTHETICAL 16.7 KD P	1.05e-26
29	256	7.9	389	2	Q54543 ASPARTATE AMINOTRANSFERASE	1.05e-25
30	250	7.8	373	1	Q30304 ASPARTATE AMINOTRANSFERASE	1.47e-25
31	249	7.7	383	2	Q31028 ASPARTATE AMINOTRANSFERASE	2.89e-25
32	242	7.5	401	1	P95957 AMINOTRANSFERASE.	4.89e-24
33	235	7.3	435	10	Q96413 ACC SYNTHASE.	1.02e-22
34	224	7.0	482	10	Q82443 ALANINE AMINOTRANSFERASE	1.16e-20
35	225	7.0	518	10	Q43753 1-AMINOCYCLOPROPANE-1-	7.58e-21
36	216	6.7	388	2	P96847 HYPOTHETICAL 41.0 KD P	3.50e-19
37	216	6.7	422	4	Q16773 GLUTAMINE--PHENYLPIRUV	3.50e-19
38	208	6.5	390	2	Q53620 AMINOTRANSFERASE.	1.02e-17
39	208	6.5	457	11	Q08415 MULTIFUNCTIONAL AMINOT	1.02e-17
40	211	6.5	482	2	P96681 YDEF PROTEIN.	2.89e-18
41	207	6.4	465	2	P96663 YDEF PROTEIN.	1.55e-17
42	203	6.3	444	10	Q43756 1-AMINOCYCLOPROPANE-1-	8.23e-17
43	203	6.3	493	10	Q42668 1-AMINOCYCLOPROPANE-1-	8.23e-17
44	200	6.2	409	5	O61103 HYPOTHETICAL 44.4 KD P	2.86e-16
45	200	6.2	497	5	O61101 HYPOTHETICAL 55.0 KD P	2.86e-16

ALIGNMENTS

RESULT 1	PRELIMINARY;	PRT;	389 AA.
ID 049451			
AC 049451			
DT 01-JUN-1998	(TREMBREL. 06, CREATED)		
DT 01-JUN-1998	(TREMBREL. 06, LAST SEQUENCE UPDATE)		
DT 01-AUG-1998	(TREMBREL. 07, LAST ANNOTATION UPDATE)		
DE TYROSINE TRANSAMINASE-LIKE PROTEIN (EC 2.6.1.5)			
GN F2109.100			
OS ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).			
OC EUKARYOTA; VIRIDIPLANTAE; STREPTOPHYTA; EMBRYOPHYTA; TRACHEOPHYTA;			
OC EUPHYLLOPHYTES; SPERMATOPHYTA; MAGNOLIOPHYTA; EUDICOTYLEDONS; ROSIDAE;			
OC CAPPARALES; BRASSICACEAE; ARABIDOPSIS.			
RN [1]			
RP SEQUENCE FROM N.A.			
RA BEVAN M., KOETTER P., HEMPEL S., ENTIAN K.-D., HOHEISEL J.,			
RA MEWES H.W., MAYER K., SCHUELLER C.;			
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN [2]			
RP SEQUENCE FROM N.A.			
RA EU ARABIDOPSIS SEQUENCING PROJECT;			
RL SUBMITTED (APR-1998) TO EMBL/GENBANK/DBJ DATA BANKS.			
CC -1- CATALYTIC ACTIVITY: L-TYROSINE + 2-OXOGLUTARATE =			
CC 4-HYDROXYPHENYLPIRUVATE + L-GLUTAMATE.			
CC -1- COFACTOR: PYRIDOXAL-PHOSPHATE.			
DR EMBL; AL021749; E1250059; -			
KW TRANSFERASE; AMINOTRANSFERASE.			
SQ SEQUENCE 389 AA; 43018 MW; D4ECDB9F CRC32;			
Query Match 39.6%; Score 1275; DB 10; Length 389;			
Best Local Similarity 47.5%; Pred. No. 2.31e-248;			
Matches 170; Conservative 89; Mismatches 93; Indels 6; Gaps 6;			
Db 16 TQODETDSVWF-RGSNA-AKASS-VTMGVIVYKLFDECSLDVKKPLPLAHDPSV 72			
QY 31 SNGHAAAAVEMFAKGKGGILATGAKNSIRAIKYSASVEESGPRVPLAHDPSV 90			
Db 73 YPCYRTSILVENAVDVLRSRGSNSTGPAAGILPARQAVADYVNRDLTKNKPNDVFTV 132			
QY 91 FPAFRTAVEAEDAAVALRTGQFNCVACVGLPAARSVAEHLSSQGVPKLSADDDVFLTA 150			
Db 133 GCNQGVTEVQLSLAR-PNANILLPRPSYPHYEARAVYSGLEVRKFDLLPERKEWEIDLPGI 191			
QY 151 GGTQAEVIVPVLAAQTAGANILLPRFGYNYEARAAFNKLEVRHFDLIPDKGWEIDISL 210			

2

"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus";
 NATURE 392:353-358(1998).
 [2]

RP SEQUENCE FROM N.A.

RC STRAIN-VF5;
 RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
 RA GRAHAM D.E., OVERBECK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
 RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.,
 RL SUBMITTED (JUL-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: AE000766; G2984217;
 KW TRANSFERASE; AMINOTRANSFERASE.
 SQ SEQUENCE 394 AA; 43777 MW; B9D83011 CRC32;

Query Match 12.5%; Score 403; DB 2; Length 394;

Best Local Similarity 29.1%; Pred. No. 3.15e-56;

Matches 106; Conservative 87; Mismatches 145; Indels 26; Gaps 25;

Db 42 PFDTPDFKEACIRALREGKTK-YAPSAGIPELREAIKELKENKVEYK-PSEIV-VS 98
 QY 92 PAFRTAVEAEDAAALRTGQFCYAAAGVGLPAARSVAEHL-SQG-VYPKLSADDDVFLT 149
 Db 99 AGAKMVLFIEMAILDE--GDEVLLSPYVWVYPEQIRFEGGVPV-EVPLKKEKGQLSL 155
 QY 150 AGTQAI-EVILPVLAQTAGANLLPRPGVYNEARAF-NKLEVRHFDLIPDKGWEIDI 207
 Db 156 EDVKERVTER-TRAIVINSPNPTGAVYEEELKIAEFCVERGFIIFISDECVEYFVGD 214
 QY 208 DSL-ESIADKNTAMVILNPNPCGVSVDYDLAKVAEYARKGLVIADEVYKGLVLS 266
 Db 215 AKFVSPASFSDEKNTFTVAFPSKYSMTGNRIGTVA-C-PEEY-AKV-IA-SLNS-OS 268
 QY 267 APFIPMGVFGH-IAPY-LSIGLSKSWIVPGWRLGVAVYDPTKILEKTKISTITNYLN 324
 Db 269 VS-NVTTFQYAGAL-EALKNPKSKDVNEMRNFERRRTAVEELSKIPGMDVV-KPEGA 325
 QY 325 VETDPATFVQ-RALPKILENTRK-ADFFKRIIGLLKESSEICYREIKENKIYTCPHKPEGS 382
 Db 326 FYIFPDPSAYA-EKLGDDVKLSEFLLEKAKVAVVPGSAFCAPGFLRLSYALSEERLVEGI 384
 QY 383 MFVMVKLNHLLEEIHDDIDFCKLAKEESVILCPGSLGMENWVRITACVPSSLDGL 442
 Db 385 RIK 388
 QY 443 ERVK 446

RESULT 9

ID O88124 PRELIMINARY; PRT; 402 AA.

AC O88124;

DT 01-NOV-1998 (TREMBLREL. 08, CREATED)

DT 01-NOV-1998 (TREMBLREL. 08, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE PUTATIVE AMINOTRANSFERASE.

GN STGA.

OS STREPTOMYCES ANULATUS.

OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;

OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.

RN [1]

RP SEQUENCE FROM N.A.

RA TERCERO J.A., ESPINOSA J.C., JIMENEZ A.;

RT "StgR, a new Streptomyces alboniger member of the Lysr family of

transcriptional regulators."

RL SUBMITTED (JUN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.

DR EMBL: AJ006517; E1318411;

DR EMBL: AJ005198; E1318407;

KW TRANSFERASE; AMINOTRANSFERASE.

SQ SEQUENCE 402 AA; 44414 MW; 5CD3256A CRC32;

Query Match 12.4%; Score 401; DB 2; Length 402;

Best Local Similarity 26.7%; Pred. No. 8.18e-56;

Matches 97; Conservative 94; Mismatches 152; Indels 20; Gaps 17;

Db 24 ANALEEAG-HSVLRNLTGNPALF-GFEAPEEIVQDMIRMLPOAH-G-YTDSRGVLSARRA 79
 QY 69 SASVESGPRPVLPLAHGDPSPVPAFTAVEAEDAAALRTGQFCYAAAGVGLPAARSA 128
 Db 80 VAQRYOALGLD-EVSVDDVFLGNGVSELVTMAVQALLE-DGDEILIPAPDFPLWTAVTTL 137
 QY 129 VAEHL-SQGVYPKLSADDDVFLTAGGTQAEIVIPVLAQTAGANILLPRGYPNYEARAF 187
 Db 138 SGGKAVHYVCDEADHYPLDDMASKITQTKAVEIINET---GAVYPREILEGIDLAR 194
 QY 188 NKLEVRHFDLIPDKGWEIDIDLSLESTADKNTTAMVILNPNPCGVSYSYDHLAKVAEVAR 247
 Db 195 RHGLMVFADIEYDQILYDDAVHSHVAALAPDLVLTFCGLSKTYRVAGSRGWLVTGPR 254
 QY 248 KLIGILVIADENVYKGLVLSAPFPMGVFGHIAPVLSIGLSKSWIVPGWRLGVAVYDPT 307
 Db 255 QHARDYLEGLTMAASRLCPNAPAFIAQALGGR-QSIR-EL-TAPGGALHEQRDRAWE 311
 QY 308 KILEKTKISTITNYLNVTSD-PATF-VQEAIPKILENTKADFFKRIIGLLKESSEICYR 365
 Db 312 KLINEIPGVSCV-KPGCALYAFRLDPKV-HPHDDKEFVLDLLLOEKIQVQGT--GF-N 366
 QY 366 EIKENKIYTCPHKPEGSFMVVKLNHLLEEIHDDIDFCKLAKEESVILCPGSLGMEN 425
 Db 367 WPR 369
 QY 426 WVR 428

RESULT 10

ID O25383 PRELIMINARY; PRT; 390 AA.

AC O25383;

DT 01-JAN-1998 (TREMBLREL. 05, CREATED)

DT 01-JAN-1998 (TREMBLREL. 05, LAST SEQUENCE UPDATE)

DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)

DE SOLUTE-BINDING SIGNATURE AND MITOCHONDRIAL SIGNATURE PROTEIN (ASPB).

GN HP0672.

OS HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).

OC BACTERIA; PROTEOBACTERIA; EPSILON SUBDIVISION; HELICOBACTER GROUP;

OC HELICOBACTER.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-26695;

RX MEDLINE; 97394467.

RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,

RA FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,

RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,

RA LOFTUS B., RICHARDSON D., DODSON R., KHALAK H.G., GLODER A.,

RA MCKENNEY K., FITZGERALD L.M., LEE N., ADAMS M.D., HICKEY E.K.,

RA BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,

RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E.,

RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,

RA VENTER J.C.;

RT "The complete genome sequence of the gastric pathogen Helicobacter

pylori [published erratum appears in Nature 1997 Sep

25;389(6649):412]."

RL NATURE 388:539-547(1997).

DR EMBL: AE000580; G2313794;

DR TIGR; HP0672;

DR PFAM; PF00155; aminotran_1; 1.

KW HYPOTHETICAL PROTEIN.

SQ SEQUENCE 390 AA; 42874 MW; BAD53859 CRC32;

Query Match 11.6%; Score 374; DB 2; Length 390;

Best Local Similarity 26.7%; Pred. No. 3.06e-50;

Matches 97; Conservative 85; Mismatches 158; Indels 23; Gaps 19;

Db 40 PFDTPQAIAKALNDG-FTKYTPVAGIPELLKATAFKLKENNLDYEPNEILVNSG 98

QY 92 PAFRTAVEAEDAAALRTGQFCYAAAGVGLPAARSVAEHLSSQGVYPKLSADDDVFLTAG 151

Db 99 AKQSIFNAIQALIE-EGDEVIIPVFWTYPELVKYSYG-VYSQFIQTDEKSHFKITPKOL 156

QY 152 GTQAEVILPVLAQTAGANILLPRGYPNVYEAAAFNKLEVRHFDLIPDKG-WEIDIDSL 210
 Db 157 KDALSPK-TKMLILTPSPTGMLYSKAEVLGVKDKTKVWLSDEIYEKLYV-KGEF 214
 QY 211 -ESIAKNTTAMVIINPNPCGSVSYSLAKVAEYARKLGLVIADEYVGLVLSAPF 269
 Db 215 VSCAAVSEEMKRTITISGLSKSVAMTGRMGVAAASKKLVKLMNLSQOCTSNINSIT 274
 QY 270 IP-MGVFGHIA-PVLSIGLSKSWIVPGWRLGWAVYDFTKLETKISTSTYNLNVST 327
 Db 275 QMASIVALEGLVDKEIETMRQAFERRC-DL--AHAKI--NAI-GG--LN-ALKPDGAFYL 325
 QY 328 DPATFVQ-EAL-PKILENTKADFKRIIGLLKESSEICVREIKENKIYTCPHKPEGSMEV 385
 Db 326 FTHIG-SLCGG--DSNRFCHELLEKGVALVPCKAFGLGYVRLSFACSEEOIEKGIERI 382
 QY 386 MYKLNJHLLEIHHDDIDFCCKLAKEESVILCPGSLVGMENWVRITFACVPSSLDQGLERV 445
 Db 383 ARF 385
 QY 446 KSF 448
 RESULT 11
 ID Q05237 PRELIMINARY; PRT; 357 AA.
 AC Q05237;
 DT 01-JUL-1997 (TREMBLREL. 04, CREATED)
 DT 01-JUL-1997 (TREMBLREL. 04, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
 DE HYPOTHETICAL 39.5 KD PROTEIN.
 GN YUGH.
 OS BACILLUS SUBTILIS.
 OC BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;
 OC BACILLUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA OUEGA B., KONINGSTEYN G.;
 RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [2]
 RP SEQUENCE OF 1-214 FROM N.A.
 RC STRAIN=168;
 RA DANCHIN A.;
 RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA OUEGA B.;
 RL SUBMITTED (APR-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE; 98044033.
 RA KUNST F., OGASAWARA N., MOSTER I., ALBERTINI A.M., ALLONI G.,
 RA AZEVEDO V., BERTERO M.G., BESSIERES P., BOLOFIN A., BORCHERT S.,
 RA BORRIS R., BOURSIER L., BRANS A., BRAUN M., BRIGNELL S.C., BRON S.,
 RA BROUTLETT S., BRUSCHI C.V., CALDWELL B., CAPUANO V., CARTER N.M.,
 RA CHOI S.K., CODANI J.J., CONNERTON I.F., CUMMINGS N.J., DANIEL R.A.,
 RA DENIZOT F., DEVINE K.M., DUSTERHOFT A., EHRLICH S.D., EMERSON P.T.,
 RA ENTIAN K.D., ERRINGTON J., FABRET C., FERRARI E., FOULGER D.,
 RA FRITZ C., FUJITA M., FUJITA Y., FUNA S., GALIZZI A., GALLERON N.,
 RA GHIM S.Y., GLASER P., GOFFEAU A., GOLIGHTLY E.J., GRANDI G.,
 RA GUISEPPI G., GUY B.J., HAGA K., HALECH J., HARWOOD C.R., HENAUT A.,
 RA HILBERT H., HOISAPPEL S., HOSONO S., HULLO M.F., ITAYA M., JONES L.,
 RA JORIS B., KARAWATA D., KASAHARA Y., KLAERR-BLANCHARD M., KLEIN C.,
 RA KOBATASHI Y., KOETTER P., KONIGSTEIN S., LAUBER J., LAZAREVIC V.,
 RA KURITA K., LAPIDUS A., LARDINOIS S., LAUBER J., LAZAREVIC V.,
 RA LEE S.M., LEVINE A., LIU H., MASUDA S., MAUEL C., MEDIGUE C.,
 RA MEDINA N., MELLADO R.P., MIZUNO M., MOESTL D., NAKAI S., NOBACK M.,
 RA NOONE D., O'REILLY M., OGAWA K., OGIMARA A., OUEGA B., PARK S.H.,
 RA PARRO V., POHL T.M., PORTETELLE D., PORWOLLIK S., PRESCOTT A.M.,
 RA PRESCAN E., PUJIC P., PURNELLE B., RAPOPORT G., REY M., REYNOLDS S.,
 RA RIEGER M., RIVOLTA C., ROCHA E., ROCHE B., ROSE M., SADAI E.,

RA SATO T., SCANLAN E., SCHLEICH S., SCHROETER R., SCOFFONE F.,
 RA SERIGUCHI J., SEKOWSKA A., SEROR S.J., SERROR P., SHIN B.S., SOLDI B.,
 RA SOROKIN A., TACCONI E., TAKAGI T., TAKAHASHI H., TAKEMARU K.,
 RA TAKEUCHI M., TAKAKASHI A., TANAKA T., TERPSTRA P., TOGNONI A.,
 RA TOSATO V., UCHIYAMA S., VANDENBOL M., VANNIER F., VASSAKOTI A.,
 RA VIARI A., WAMBUTT R., WEDLER E., WEDLER H., WEITZENEGER T.,
 RA WINTERS P., WIPAT A., YAMAMOTO H., YAMANE K., YASUMOTO K., YATA K.,
 RA YOSHIDA K., YOSHIKAWA H.F., ZUMSTEIN E., YOSHIKAWA H., DANCHIN A.;
 RT "The complete genome sequence of the gram-positive bacterium Bacillus
 subtilis.";
 RL NATURE 390:249-256(1997).
 RN [5]
 RC SEQUENCE FROM N.A.
 RC STRAIN=168;
 RA KUNST F., OGASAWARA N., YOSHIKAWA H., DANCHIN A.;
 RL SUBMITTED (NOV-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 DR EMBL; Z93934; E311527; -.
 DR EMBL; Z99120; E1184218; -.
 DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
 DR PFAM; PF00155; aminotran_1; 1.
 KW HYPOTHETICAL PROTEIN; PYRIDOXAL PHOSPHATE.
 SQ SEQUENCE 357 AA; 39461 MW; FD6B02F9 CRC32;
 Query Match 11.4%; Score 368; DB 2; Length 357;
 Best Local Similarity 29.8%; Pred. No. 5,20e-49;
 Matches 64; Conservative 59; Mismatches 83; Indels 9; Gaps 9;
 Db 38 PDFVTAWNVREASILSLEQG-YTSTYANAGLYSLREEISRYLSNRFDSLVS-PDNEILVT 95
 QY 92 PAFTRAEADDAVAALRTGQFNCAAGVGLPAARSVAEHL-S-Q-GVPYKLSADDDVELT 149
 Db 96 VGASQALDIATRAIVN-PGEVVIPEPCFVADALVSLAGGIPV-HVHTADKDGKFAITA 153
 QY 150 AGGTQAEIIVIPVLAQTAGANILLPRGYPNVEAAAFNK-LEVRHFDLIPDKGWEIDID 208
 Db 154 DFEAAVTEKTKAILICSPNPTGTSYVSKELNEIAEFAKKHVDVIVLADEIYAELTYDEE- 212
 QY 209 SLESTADKNTTAMVIINPNPCGSVSYDHLAKVAEARKLGLVIADEVYKLVLSGAP 268
 Db 213 FTSIALPGMKERTVVISGFSKAFAMTGWRLGFAA 247
 QY 269 FIPMGVF-GHTAPVLSIGLSKSWIVPGWRLGWA 302
 RESULT 12
 ID Q60013 PRELIMINARY; PRT; 397 AA.
 AC Q60013;
 DT 01-NOV-1996 (TREMBLREL. 01, CREATED)
 DT 01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
 DE ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1).
 GN AAT.
 OS STREPTOMYCES VIRGINIAE.
 OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
 OC ACTINOMYCETALES; STREPTOMYCINAE; STREPTOMYCETACEAE; STREPTOMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA KATAYAMA M., SAKAI Y., OKAMOTO S., IHARA F., NIHIRA T., YAMADA Y.;
 RT "Gene organization in the ada-rpl region of the Streptomyces
 virginiae chromosome.";
 RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 DR EMBL; D50624; D1009940; -.
 DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
 DR PFAM; PF00155; aminotran_1; 1.
 KW TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
 SQ SEQUENCE 397 AA; 42381 MW; 9240ED06 CRC32;

```

Query Match      11.3%; Score 365; DB 2; Length 397;
Best Local Similarity 28.5%; Pred. No. 2.14e-48;
Matches 84; Conservative 76; Mismatches 118; Indels 17; Gaps 16;

Db 25 AGRPVGAGGPD-FPT-PDYI-VEAAVEAC-RNPKYHRYTPAGGLPELKAIAAKTL 80
QY 75 SGRPVLPLAHGDPSPVFPFAFRTAVEADEAVAAALRTGQFCYAAAGVGLPAARSAVAEHL 134

Db 81 RDSGEVEASOVLVTNGKQAIYEAFAAIL-D-PGDEVIVPAPYWTYTPESIRLAG-GVP 137
QY 135 QGVPYKLSADDDVLTAGGTQAI-EVPIVLAQTAGANILLPRGYPNYEARAAFNKLEVR 193

Db 138 -VDVADEITGYRVSVEQLEAARTERTKVLFVSPNPGTSVSYSEADAKAIGWAHGL 196
QY 194 HFDLIPD--KGWEIDIDSLESIAKNTAMVINPNPCGVSYSYDHLAKVAEVARGLGI 251

Db 197 WVLTDIEIHLVYGEAKFTSLPLVLPALRDKCIIVNGVAKTYAMTGRVGVW-IAQDVI 255
QY 252 LVIADEVYGLVLSGAPFIPMGVFGH-I-APVLSIGLSKSWIVPGWGLWVAVYDPTKI 309

Db 256 KAATINQSHATSNVSNVAOVAALAAVSGNLDVAEMRKA-FDRRRQTMVKMLNEI 309
QY 310 LEXTKISTSTINVL-NVSTDPA-TFQVEALPKILENTKADFFRIIGLLKESSEI 362

RESULT 13
ID O53870 PRELIMINARY; PRT; 397 AA.
AC O53870;
DT 01-JUN-1998 (TREMELREL. 06, CREATED)
DT 01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)
DE PUTATIVE AMINOTRANSFERASE.
GN MT043.51C.
OS MYCOBACTERIUM TUBERCULOSIS.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; CORINEBACTERIACEAE; MYCOBACTERIACEAE; MYCOBACTERIUM.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA HAMILIN N., CHURCHER C.M.;
RL SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RA COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (FEB-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96181548.
RA PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELIA L.,
RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA COLE S.T.;
RT "An integrated map of the genome of the tubercle bacillus,
RT Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
RT leprae."
RL PROC. NATL. ACAD. SCI. U.S.A. 93:3132-3137(1996).
DR EMBL; AL022004;
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 397 AA; 42209 MW; 447498CB CRC32;

Query Match      11.2%; Score 361; DB 2; Length 397;
Best Local Similarity 30.9%; Pred. No. 1.41e-47;
Matches 68; Conservative 56; Mismatches 87; Indels 9; Gaps 9;

Db 57 YPPGCSAPLRRAIAQRHRRHFVDYD-PETEVLTIVTGATEAIAAAVLGIVE-PGSEVLL 114
QY 116 YAAGVGLPAARSAVA-EHLSQ-GVPYKLSADDDVLTAGGTQAIETIPIVLAQTAGANILL 173

Db 115 IEPFYDSYSPVVMAGARHRTVPLVDGRGFDALDARRAVTPTRTRALIINSPHNTGCA 174
QY 174 PRGYPNYEARAAFNKLEVRHFDLIPD-KGWEIDIDSLESIAKNTAMVINPNPCGS 232

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Db 175 VLSATELAAAEIAVAANLWVITDEVYEHVLFDFHARHLPLAGFDGMAERTITISSAAKMF 234
QY 233 VYSYDHLAKVAEVARKLIVIADEVYKLVLSAFAFIPMGVFGHIA-PVLSIGLSKSW 291

Db 235 NCTGWKIGW-A-CGPAELIAGVRAAKOYLSYVGAGFPQPA 272
QY 292 IVPGWRLGWAVVDPTKILEKTISTITNYLNVST-DPA 330

RESULT 14
ID O54170 PRELIMINARY; PRT; 382 AA.
AC O54170;
DT 01-JUN-1998 (TREMELREL. 06, CREATED)
DT 01-JUN-1998 (TREMELREL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMELREL. 08, LAST ANNOTATION UPDATE)
DE AMINOTRANSFERASE.
GN SC7HL.11.
OS STREPTOMYCES COELICOLOR.
OC BACTERIA; FIRMICUTES; ACTINOBACTERIA; ACTINOBACTERIDAE;
OC ACTINOMYCETALES; STREPTOMYCINEAE; STREPTOMYCETACEAE; STREPTOMYCES.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA MURPHY L., HARRIS D.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL SUBMITTED (JAN-1998) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE; 97000351.
RA KINASHI H., HOPWOOD D.A.;
RA REDENBACH M., KIESER H.M., DENAPATE D., EICHNER A., CULLUM J.,
RT "A set of ordered cosmids and a detailed genetic and physical map for
RT the 8 Mb streptomycetes coelicolor A3(2) chromosome."
RL MOL. MICROBIOL. 21:77-96(1996).
DR EMBL; AL021411; E1245740;
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 382 AA; 40860 MW; 9FC8F75A CRC32;

Query Match      10.6%; Score 342; DB 2; Length 382;
Best Local Similarity 26.1%; Pred. No. 1.03e-43;
Matches 80; Conservative 83; Mismatches 131; Indels 13; Gaps 10;

Db 1 MIATPPASRIAEELRRSRPALAPPPGAVSLAMGEPD-FPTPTVYQA--AVSA-LREG 56
QY 52 LATTGAKNSIRAIRYKISAVEESGPRVPLPLAHGDPSPVFPARTAVEADEAVAAALRTG 111

Db 57 HPH-YADQGLRELRAALARPERRPGAWDADDVLVTHGATAAALAAV-LATVGPGRV 114
QY 112 QFNCTAAGVGLPAARSAVAEHLISQGVYKLSADDDVLTAGGTQAIETIPIVLAQTAGANI 171

Db 115 VYPEPAYSIALDLVLAGGTGVFVPLAPLHW--DLDALAAALP-GAAMMIFSNPSNPTG 171
QY 172 LIPRGYPNYEARAAFNKLEVRHFDLIPDKGWEIDIDSLESIAKNTAMVINPNPCG 231

Db 172 IVHREELKGLLDGTDVLVVSDEAYHRLAYPGHEPVSALEIESLRGRTVYVOTFSK 231
QY 232 SVYSYDHLAKVAEVARKLIVIADEVYKLV-L-GSAPFIPMGVFGHIAFVLSIGLSKS 290

Db 232 YAMTGRVGYLI--GPREVLDAAQVHRTWNGSLNTAVOHAALALDLPDGVGAMADRY 289
QY 291 WIVPGWRLGWAVYDPTKILEKT-KISTSTINLYNVSTDPATFVQEPALPKILENTKADFF 349

Db 290 RORRDIV 296
QY 350 KRIIGLL 356

RESULT 15

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ID O58489 PRELIMINARY; PRT; 391 AA.
AC O58489;
DT 01-AUG-1998 (TREMBREL. 07, CREATED)
DT 01-AUG-1998 (TREMBREL. 07, LAST SEQUENCE UPDATE)
DT 01-JAN-1999 (TREMBREL. 09, LAST ANNOTATION UPDATE)
DE 391AA LONG HYPOTHETICAL ASPARTATE AMINOTRANSFERASE.
GN PH0771.
OS PYROCOCUS HORIKOSHII.
OC ARCHAEA; EURYARCHAEOTA; THERMOCOCCALES; THERMOCOCCACEAE; PYROCOCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE; 98344137.
RA KAWARABAYASHI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
RA YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,
RA SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
RA KIKUCHI H.;
RT "Complete Sequence and Gene Organization of the Genome of a
RT Hyper-thermophilic Archaeobacterium, Pyrococcus horikoshii Ot3.";
RL DNA RES 5:55-76(1998).
DR EMBL; AP000003; D1030806;
KW TRANSFERASE; AMINOTRANSFERASE.
SQ SEQUENCE 391 AA; 44565 MW; A549ACDA CRC32;

Query Match 10.2%; Score 330; DB 1; Length 391;
Best Local Similarity 28.4%; Pred. No. 2.75e-41;
Matches 103; Conservative 82; Mismatches 148; Indels 30; Gaps 29;

Db 42 PDFDTPKNKEAAKRALDEG-WTHYTPNAGIPELREAVVEYKKFYGIDIEVENVIITAG 100
QY | | : : | | | | : : | | : : | | : : | | : : | | : : | | : : | |
| | : : | | | | : : | | : : | | | | : : | | : : | | : : | | : : | |
92 PAERTAVEAEDAVAAALRTQFNCYAAGVGLPAARSAVAEHL SQGVPKLSADDDVELTAG 151
Db 101 AYECTYLAPESELLER-GDEVIIIPDPAFVSVAEDAKVAEAK-PVR-IPLRENNFLDPNE 157
QY : : : : | : : : | : : : | : : | | : : | | : : | | : : | | : :
152 GTOAIEVIIPVLAOTAGANILLPRGYPNY-E-ARAFNKLVEVRHFDLIPDKGWEIDIDS 209
Db 158 LLEKIS-KNTR-MIVINYPNNPTGATLD-KELAKTIADIAEDYNIYILSDPEYEHFIYED 214
QY | | : : | | : : | | | | | | : : | | : : | | : : | | : : | | : :
| | : : | | : : | | | | | | : : | | : : | | : : | | : : | | : :
210 L-ESIADKNVTAMVIN-PNNPCGSVYSYDHLAK-VAEVARKLGILVIADDEVYKLVLS 266
Db 215 AKHYPMIKFAPENTILA-NSFSKTFAMTGWRLGFV-Y-APSQVI-K-EM-TKLHAYV-IG 267
QY | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
| | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : :
267 APFIPMGVFGHIAPLVLSIGSLSKSWIVPGWRLGWAVYDPTKILEKTISTITNLNVS 326
Db 268 -NVASFVQIAGIEAL-RS-EESWKAYEEMKKEYNERRKIVVKKLKNMPGKVKPEKGFY 324
QY : : | | | | | | : : : : | | : : | | : : | | : : | | : : | | : :
327 TDPATFVQEARLPKILENTKADFFKRIGLKESSICEYREIKENKYITCPH-K-PEGSMF 384
Db 325 VFPNIS-G--TGMSSSE-KFSEWLLKARVVVVPITGAFGRMGEGYVRISYATSKELIEM 380
QY | : : : | : : | | : : | | : : | | : : | | : : | | : : | | : :
| : : : | : : | | : : | | : : | | : : | | : : | | : : | | : :
385 VMVKLNHLLEEIHDDIDFCCKLAKEESVILCPGSLV-G-M-ENWVRITFACVPSSIQDGL 442
Db 381 NRI 383
QY : | :
443 ERV 445

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Search completed: Fri Oct 1 13:51:35 1999
Job time : 39 secs.

WISORLH (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Oct 1 13:51:53 1999; MasPar time 22.78 Seconds
Tabular output not generated. 810.770 Million cell updates/sec

Title: >US-09-026-400-2
Description: (1-461) from US09026400.pep
Perfect Score: 3223

Sequence: 1 MVHQSNGHGEAAAAANGKS.....LERVKSFQCRNKKKNSINGC 461

Scoring table: PAM 150
Gap 11

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir60
1.pir1 2.pir2 3.pir3 4.pir4

Statistics: Mean 49.862; Variance 105.736; scale 0.472

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	920	28.5	454	1	XNRTY	2.11e-146
2	914	28.4	454	2	tyrosine transaminase	3.08e-145
3	495	15.4	429	2	S10887	2.11e-65
4	439	13.6	401	2	H70506	4.22e-55
5	410	12.7	405	2	D71003	7.94e-50
6	403	12.5	394	2	H65000	1.47e-48
7	394	12.2	402	2	A70469	6.17e-47
8	376	11.7	390	2	S07088	1.05e-43
9	374	11.6	390	2	H71909	2.40e-43
10	368	11.4	357	2	H64603	2.83e-42
11	368	11.4	375	2	G70010	2.83e-42
12	361	11.2	397	2	A64300	5.00e-41
13	358	11.1	392	2	B70815	1.71e-40
14	330	10.2	391	2	A38621	1.50e-35
15	330	10.2	393	2	E71125	1.50e-35
16	323	10.0	379	2	C69591	2.52e-34
17	308	9.6	412	2	A69516	1.03e-31
18	299	9.3	389	2	E71718	3.69e-30
19	299	9.3	389	2	E71009	2.48e-30
20	300	9.3	392	2	C69672	1.21e-29
21	296	9.2	383	2	S45923	1.80e-29
22	295	9.2	385	2	JC5775	2.68e-29
23	294	9.1	374	2	G59119	

24 294 9.1 507 2 S52677 probable membrane pro 2.68e-29
25 290 9.0 390 2 F69452 aspartate aminotransf 1.30e-28
26 285 8.8 400 2 A47094 aspartate transaminas 9.33e-28
27 277 8.6 373 2 E70338 aminotransferase (Asp 7.15e-26
28 268 8.3 432 2 F64484 alanine transaminase 7.17e-25
29 263 8.2 389 2 S74343 aspartate aminotransf 4.98e-24
30 258 8.0 444 2 S56832 kynurenine aminotrans 3.43e-23
31 256 7.9 389 2 S75949 hypothetical protein 7.41e-23
32 250 7.8 373 2 F69545 aspartate aminotransf 7.39e-22
33 242 7.5 401 2 S75385 probable aspartate tr 1.56e-20
34 241 7.5 410 2 A40658 aspartate transaminas 2.28e-20
35 235 7.3 386 2 F64793 ybdl protein - Escher 2.20e-19
36 231 7.2 482 2 S42535 alanine transaminase 9.90e-19
37 227 7.0 516 2 S19252 1-aminocyclopropane-1 4.42e-18
38 225 7.0 518 2 S31442 1-aminocyclopropane-1 9.33e-18
39 222 6.9 387 2 S29934 aminotransferase patB 2.85e-17
40 221 6.9 399 2 S39740 aspartate aminotransf 4.13e-17
41 216 6.7 388 2 C70605 probable aminotransfe 2.62e-16
42 216 6.7 422 2 S52790 glutamine-phenylpyru 2.62e-16
43 217 6.7 482 2 S38429 alanine transaminase 1.81e-16
44 211 6.5 385 2 S8456 histidinol-phosphate 1.65e-15
45 211 6.5 482 2 B69780 transcription regulat 1.65e-15

ALIGNMENTS

RESULT 1
ENTRY XNRTY #type complete
TITLE tyrosine transaminase (EC 2.6.1.5) - rat
ALTERNATE_NAMES tyrosine aminotransferase
ORGANISM #formal_name Rattus norvegicus #common_name Norway rat
DATE 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 26-Feb-1999
ACCESSIONS A23310; A31804; JN0343; A48430; S18308; S17849
REFERENCE A23310
#authors Grange, T.; Guenet, C.; Dietrich, J.B.; Chasserot, S.; Fromont, M.; Befort, N.; Jami, J.; Beck, G.; Pictet, R.
#journal J. Mol. Biol. (1985) 184:347-350
#title Complete complementary DNA of rat tyrosine aminotransferase messenger RNA. Deduction of the primary structure of the enzyme.
#cross-references MIMD:85293103
#accession A23310
#molecule_type mRNA
#residues 1-454 #label GRA
#cross-references EMBL:X02741; NID:957327; PID:957328
#note part of this sequence was confirmed by protein sequencing
REFERENCE A31804
#authors Hargrove, J.L.; Scoble, H.A.; Mathews, W.R.; Baumstark, B.R.; Biemann, K.
#journal J. Biol. Chem. (1989) 264:45-53
#title The structure of tyrosine aminotransferase. Evidence for domains involved in catalysis and enzyme turnover.
#cross-references MIMD:89079691
#accession A31804
#molecule_type mRNA
#residues 226-284, 'G', 286-358, 'DL', 361-444, 'D', 446-454 #label HAR
#cross-references GB:M18340
#note the authors translated the codon GGG for residue 285 as Pro
#note part of this sequence was confirmed by protein sequencing
REFERENCE JN0343
#authors Zelenin, S.M.; Popova, V.S.; Morozov, I.V.; Tishkav, V.I.; Egorov, A.M.; Mertvetsov, N.P.
#journal Bioorg. Khim. (1991) 17:994-996
#title Nucleotide sequence of an EcoRI-fragment of the rat tyrosine aminotransferase gene determined on the automated sequencer "Applied Biosystems" model 370A.
#cross-references MIMD:92172066
#accession JN0343
#molecule_type DNA

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# #residues      385-454 ##label ZEL
##experimental_source liver
REFERENCE A48430
#authors Morozov, I.V.; Mishin, V.P.; Zelenin, S.M.; Popova, V.S.;
          Mertvetsov, N.P.
#journal DNA Seq. (1990) 1:151-155
#title Nucleotide sequence of rat liver tyrosine aminotransferase
          gene fragment.
#cross-references MUID:92190544
#accession A48430
##status preliminary
##molecule_type DNA
##residues 190-284,'L',286-386 ##label MOR
##cross-references GB:X15590; NID:g57845; PID:g1334238
##experimental_source liver
##note sequence extracted from NCBI backbone (NCBIN:89708,
          NCBIP:89709)

REFERENCE S18308
#authors Lorber, B.; Dietrich, J.B.; Kern, D.
#journal FEBS Lett. (1991) 291:345-349
#title Isolation and characterization of active N-terminal truncated
          apo- and holoenzyme of mammalian liver tyrosine
          aminotransferase.
#cross-references MUID:92038067
#accession S18308
##molecule_type protein
##residues 38-52;58-81 ##label LOR
##experimental_source liver

REFERENCE S17849
#authors Dietrich, J.B.; Lorber, B.; Kern, D.
#journal Eur. J. Biochem. (1991) 201:399-407
#title Expression of mammalian tyrosine aminotransferase in
          Saccharomyces cerevisiae and Escherichia coli. Purification
          to homogeneity and characterization of the enzyme
          overproduced in the bacteria.
#cross-references MUID:92037592
#accession S17849
##status not compared with conceptual translation
##molecule_type DNA
##residues 1,'V',3-10 ##label DIE
##experimental_source liver

GENETICS 408/3
#introns
CLASSIFICATION superfamily mammalian tyrosine aminotransferase
KEYWORDS acetylated amino end; aminotransferase; homodimer;
          phosphoprotein; pyridoxal phosphate

FEATURE
383-394
1
#region PEST sequence\
#modified_site acetylated amino end (Met) #status
          experimental\
#binding_site pyridoxal phosphate (Lys) (covalent)
          #status experimental
#length 454 #molecular-weight 50635 #checksum 7044

SUMMARY
Query Match 28.58; Score 920; DB 1; Length 454;
Best Local Similarity 34.38; Pred. No. 2,11e-146;
Matches 137; Conservative 117; Mismatches 135; Indels 11; Gaps 10;

Db 49 SNKTFNPIRAIVDNMKYQPNPKTVISLSIGDPTVFNGNLTPDEVTQAMKDALDSKGYNG 108
    :::::| | : - : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 57 AKNSIRAIRKYISA-SVEESGPRPVLPFLANGDSPVPFPAFTVAEADAARLRGTQCNC 115
    :::::| | : - : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 109 YAPSIGYLSRREEVASYHHCHERAP--LEAKDVILTSGCSQAELCLAVLAN-PGONILIP 165
    ||:::| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 116 YAAGVGGLPAARSAAAEHL-SQGVPYKLSADVDVFLTAGTQTAEIIVPQLAQTAGANILLP 174
    ||:::| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 166 RPGSLRYTLAESMGIEVKLYNLLPEKSWEIDIKLESIDEKTACLVYNNPSNPCGSVF 225
    ||:::| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 175 RPQYPNYEARAFNFKNLEVRHFDLPDKGWIEDIDSLESTADKNWTAMVIINFNFCGSVY 234
    ||:::| | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 236 SKRHLOKTLIAVERQCVPILADEFITGDWDFSDCKYEPPLANLTNTNPILSCGGIAKRWLVP 285
Ov 235 SYDHIAKVAEARKGLITVLTADEVYKLGVSAPPFTPMGVFGHIAPVLISGLSKSWIVP 294
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```
QY 251 ILVIADEVYKVLGSAPIPMGVFGHIAPIVLSIGSLSKSWIVPGWRLGWAVYDPTKIL 310
Db 262 SEVREAIKLRIRICPNTPGQFA--AIAG-LTGM-DYLKEYMKLKERDFIYKRLNE 317
QY 311 ETKTKISTTNVLNSTD-PATFVQEQALPKILENTKADFFKRIIGLLKESSEICYREIKE 369
Db 318 IFCIS-TTRQGAIFYIPRIE 337
QY 370 NKYITCPHRPEGSFVWVKLN 390

RESULT 5
ENTRY H65000 #type complete
TITLE hypothetical protein b2290 - Escherichia coli (strain K-12)
ORGANISM #formal_name Escherichia coli
DATE 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change
14-Nov-1997
ACCESSIONS H65000
REFERENCE A64720
#authors Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.;
Burland, V.; Riley, M.; Collado-Vides, J.; Glasner, J.D.;
Rode, C.K.; Mayhew, G.F.; Gregor, J.; Davis, N.W.;
Kiripatrick, H.A.; Goeden, M.A.; Rose, D.J.; Mau, B.; Shao,
Y.
#journal Science (1997) 277:1453-1462
#title The complete genome sequence of Escherichia coli K-12.
#cross-references MUID:97426617
#accession H65000
#status preliminary; nucleic acid sequence not shown;
translation not shown
#molecule_type DNA
#residues 1-405 #label BLAT
#cross-references GB:AE000318; GB:U00096; NID:g1788623; PID:g1788627;
UWGP:b2290
#experimental_source strain K-12, substrain MG1655
SUMMARY #length 405 #molecular-weight 45517 #checksum 4760
Query Match 12.7%; Score 410; DB 2; Length 405;
Best Local Similarity 27.3%; Pred. No. 7.94e-50;
Matches 100; Conservative 94; Mismatches 154; Indels 18; Gaps 18;
Db 17 IRGPVLEAKRLEEGNK-VLKNIGNPAPF-GFDAPDEILVDVIRNLPTAQ-G-YCDSK 72
QY 61 IRAIRYKISAVESESGRPVPLAHGDPVFPPTAIVAEADAVAAALRTGQFNCAAGV 120
Db 73 GLXSARKAIMQHVQAGMR-DVTVEDIYIGNGVSELIVQAMQALLNS-GDEMLVPADYP 130
QY 121 GLPARSAVAEHL-SQGVYPKLSADDFLTAGGTQATEIIPVLAQTAGANILLPRGYP 179
Db 131 LWTAAVSLSSKAVHY-LCDESSWDFDLDIRAKITPRTRGVIINPNPTGAVYSKEL 189
QY 180 NYEARAAFNKLEVRHFLDIPDKG-WEIDISLESIADKNTAMVIINPNPCGSVSYD 238
Db 190 LMEIVEARQNLIIFADEIYDKILYDAAHSHIAPLAPDLLTIFNGLSKTYRVAFRQ 249
QY 239 LAKVAEVARKLGIIVIADEVYKVLGSAPIPMGVFGHIAPIVLSIGSLSKSWIVPGWRL 298
Db 250 GWVYLVNGPKK-HAKGYIEGLEMLASMRLCANVPQAQIAQTALGY-QSI-SEFTPG-GR 305
QY 299 GWAVYDPTKILETKIST-SITVNLNSTD-PATF-VQEQALPKILENTKADFFKRIIGL 355
Db 306 LYEORNRAMELINIPGVSCV-KRGALYMPFKIDAKRFN-IHDDQKMLVDFLQEKVLL 363
QY 356 LKESSEICYREIKENKYITCPHRPEGSFVWVKLNHLLEIEHDDIDFCCCKLAKEESVIL 415
Db 364 VQGTAF 369
QY 416 CPGSVL 421

RESULT 6
ENTRY #type complete
#formal_name Aquifex aeolicus
#sequence_revision 08-May-1998 #text_change
13-Sep-1998
ACCESSIONS A70469
REFERENCE A70300
#authors Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.
#journal Nature (1998) 392:353-358
#title The complete genome of the hyperthermophilic bacterium
Aquifex aeolicus.
#cross-references MUID:98196666
#accession A70469
#status preliminary; nucleic acid sequence not shown;
translation not shown
#molecule_type DNA
#residues 1-394 #label AOF
#cross-references GB:AE000766; NID:g2984216; PID:g2984217; GB:AE000657
#experimental_source strain VF5
GENETICS aspC1
#gene
CLASSIFICATION #superfamily aspartate transaminase
SUMMARY #length 394 #molecular-weight 43777 #checksum 8792
Query Match 12.5%; Score 403; DB 2; Length 394;
Best Local Similarity 29.1%; Pred. No. 1.47e-48;
Matches 106; Conservative 87; Mismatches 145; Indels 26; Gaps 25;
Db 42 PDFDTPDFKEACIRALREGTK-YAPSAGIPPELREATAEKLLKENKYK-PSEIV-VS 98
QY 92 PAFTVAEADAVAAALRTGQFNCAAGVGLPAARSVAEHL-SQG-VPYKLSADDFLT 149
Db 99 AGAKMVLFIIFMAILDE--GDEVLLPSPVWVYTPQIRFFGGVPV-EVPLKKEKGFQLSL 155
QY 150 AGGTOAI-EVLIIPVLAQTAGANILLPRGYPNYEARAAF-NKLEVRHFLDIPDKGWEIDI 207
Db 156 EDVKEKVTET-TKAIVINSPNPTGAVYEELKKAIEFCVERGIFIIISDECYEVYVGD 214
QY 208 DSI-ESIAKNTAMVIINPNPCGSVSYDHLAKVAEYARKLGIIVIADEVYKVLGSL 266
Db 215 AKFVSPASFDEYKNTFTVNAFSKSYMTGWRIGVVA-C-PEEY-AKV-IA-SLNS-OS 268
QY 267 APIPMGVFGH-IAPV-LSIGSLSKSWIVPGWRLGWAVYDPTKILETKISTITN 324
Db 269 VS-NVITPAQYGL-PALANPKSKDFVNMENRAFERRRTAVEELSKIFQMDVV-PREGA 325
QY 325 VSTDPAFVQ-EALPKILENTKA-DFFKRIIGLLKESSEICYREIKENKYITCPHRPEGS 382
Db 326 FYIFPDPSAVA-EKLGDDVKLSEFLLEKAKVAVVPGSAFGAPGFLRLSYALSEERLVEGI 384
QY 383 MFVWVKLNHLLEIEHDDIDFCCCKLAKEESVILCPGSLGMENWVITACVPSLLQDGL 442
Db 385 RRIK 388
QY 443 ERVK 446

RESULT 7
ENTRY #type complete
TITLE aspartate transaminase (EC 2.6.1.1) - Sulfolobus solfataricus
ALTERNATE_NAMES aspartate aminotransferase
ORGANISM #formal_name Sulfolobus solfataricus
DATE 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
13-Sep-1998
ACCESSIONS S07088; S27106; S45613
REFERENCE S07088
#authors Cubellis, M.V.; Rozzo, C.; Nitti, G.; Arnone, M.I.; Marino,
G.; Sannia, G.
#journal Eur. J. Biochem. (1989) 186:375-381
#title Cloning and sequencing of the gene coding for aspartate
aminotransferase from the thermoacidophilic archaeobacterium
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TITLE aspartate aminotransferase - Aquifex aeolicus
ORGANISM #formal_name Aquifex aeolicus
DATE 08-May-1998 #sequence_revision 08-May-1998 #text_change
13-Sep-1998
ACCESSIONS A70469
REFERENCE A70300
#authors Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.;
Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.;
Keller, M.; Aujay, M.; Huber, R.; Feldman, R.A.; Short,
J.M.; Olson, G.J.; Swanson, R.V.
#journal Nature (1998) 392:353-358
#title The complete genome of the hyperthermophilic bacterium
Aquifex aeolicus.
#cross-references MUID:98196666
#accession A70469
#status preliminary; nucleic acid sequence not shown;
translation not shown
#molecule_type DNA
#residues 1-394 #label AOF
#cross-references GB:AE000766; NID:g2984216; PID:g2984217; GB:AE000657
#experimental_source strain VF5
GENETICS aspC1
#gene
CLASSIFICATION #superfamily aspartate transaminase
SUMMARY #length 394 #molecular-weight 43777 #checksum 8792
Query Match 12.5%; Score 403; DB 2; Length 394;
Best Local Similarity 29.1%; Pred. No. 1.47e-48;
Matches 106; Conservative 87; Mismatches 145; Indels 26; Gaps 25;
Db 42 PDFDTPDFKEACIRALREGTK-YAPSAGIPPELREATAEKLLKENKYK-PSEIV-VS 98
QY 92 PAFTVAEADAVAAALRTGQFNCAAGVGLPAARSVAEHL-SQG-VPYKLSADDFLT 149
Db 99 AGAKMVLFIIFMAILDE--GDEVLLPSPVWVYTPQIRFFGGVPV-EVPLKKEKGFQLSL 155
QY 150 AGGTOAI-EVLIIPVLAQTAGANILLPRGYPNYEARAAF-NKLEVRHFLDIPDKGWEIDI 207
Db 156 EDVKEKVTET-TKAIVINSPNPTGAVYEELKKAIEFCVERGIFIIISDECYEVYVGD 214
QY 208 DSI-ESIAKNTAMVIINPNPCGSVSYDHLAKVAEYARKLGIIVIADEVYKVLGSL 266
Db 215 AKFVSPASFDEYKNTFTVNAFSKSYMTGWRIGVVA-C-PEEY-AKV-IA-SLNS-OS 268
QY 267 APIPMGVFGH-IAPV-LSIGSLSKSWIVPGWRLGWAVYDPTKILETKISTITN 324
Db 269 VS-NVITPAQYGL-PALANPKSKDFVNMENRAFERRRTAVEELSKIFQMDVV-PREGA 325
QY 325 VSTDPAFVQ-EALPKILENTKA-DFFKRIIGLLKESSEICYREIKENKYITCPHRPEGS 382
Db 326 FYIFPDPSAVA-EKLGDDVKLSEFLLEKAKVAVVPGSAFGAPGFLRLSYALSEERLVEGI 384
QY 383 MFVWVKLNHLLEIEHDDIDFCCCKLAKEESVILCPGSLGMENWVITACVPSLLQDGL 442
Db 385 RRIK 388
QY 443 ERVK 446

RESULT 7
ENTRY #type complete
TITLE aspartate transaminase (EC 2.6.1.1) - Sulfolobus solfataricus
ALTERNATE_NAMES aspartate aminotransferase
ORGANISM #formal_name Sulfolobus solfataricus
DATE 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change
13-Sep-1998
ACCESSIONS S07088; S27106; S45613
REFERENCE S07088
#authors Cubellis, M.V.; Rozzo, C.; Nitti, G.; Arnone, M.I.; Marino,
G.; Sannia, G.
#journal Eur. J. Biochem. (1989) 186:375-381
#title Cloning and sequencing of the gene coding for aspartate
aminotransferase from the thermoacidophilic archaeobacterium
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#authors

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#journal
#title
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#cross-references MUID:96337999
#accession A64300
#status preliminary; nucleic acid sequence not shown;
#molecule_type DNA
#residues 1-375 ##label BUL
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TIGR:MJ0001; PID:g1510187

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#map_position REV3343-2216
CLASSIFICATION #superfamily aspartate transaminase
KEYWORDS aminotransferase
SUMMARY #length 375 #molecular-weight 42395 #checksum 1390

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Best Local Similarity 26.3%; Pred. No. 2.83e-42;
Matches 78; Conservative 84; Mismatches 117; Indels 18; Gaps 16;

Db 33 POFDTPKHIEAAKRALDEKTH-YSPNNGIPELREISNKLKDDYNLQVDKNIIVTCG 91
QY 92 PAFRTAVEAEDAAALRTGQFCYAGVGLPAARSAVAEHLISQGVYKLSADDDVELTAG 151

Db 92 ASBALMSLMTLIDR-GDEVLIPNPFVSFUTEPAEGKKNIDL--DENFNIDLEKYK 148
QY 152 GTQAIEVILPVLQAOTAGANILLPRGYPNYEARAAFNKLEVRHFDLIPDKGWEIDISL- 210

Db 149 ESIT-KTKLIIPNSPNTGKYDKETIKGLAEADYNLIIVSDEVYDKIIYDKKHYS 207
QY 211 ESIADKNTTAMVIINPNPCGSYVSHDLAKVAEARKLILVIADEVYKLVLSGAPFI 270

Db 208 PMQ-FTDRC-IL-INGFSTYAMTGRIGYLAVIDELNKLNNMIKHQY-SPAC-A 262
QY 271 PMGVGHIAFVLSIGLSKSVIPGRLGWAVYDP-TKILEKTKISTITNLYNVSTDP 329

Db 263 TTFQAQYALAL-ALRGSG-KCEDMVREFKMRDLIYNGLKDI-FKV--NKPDGAFYI 314
QY 330 ATFVQ-EALPKILENTKADFRRKIIGLLKESSEICYREIKENKIYTCPHKPGSMFV 385

RESULT 12
ENTRY #type complete
TITLE hypothetical protein Rv0858c - Mycobacterium tuberculosis
ORGANISM (strain H37Rv)
DATE #formal_name Mycobacterium tuberculosis
17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
ACCESSION B70815
REFERENCE A70500
#authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eigmeier, K.; Gas, S.; Barry III, C.E.; Rekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, K.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.

#journal Nature (1998) 393:537-544
#title Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
#cross-references MUID:98295987
#accession B70815
#status preliminary; nucleic acid sequence not shown;
#molecule_type DNA
#residues 1-397 ##label COL
#cross-references GB:AL022004; GB:AL123456; NID:g3261550; PID:e1254000;
#experimental_source strain H37Rv

GENETICS
#gene Rv0858c
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SUMMARY #length 397 #molecular-weight 42209 #checksum 1391

Query Match 11.2%; Score 361; DB 2; Length 397;
Best Local Similarity 30.9%; Pred. No. 5.00e-41;
Matches 68; Conservative 56; Mismatches 87; Indels 9; Gaps 9;

Db 57 YFPGSGAPLRRRAIAAQRHRRHFGVDYD-PETEVLTVTGATEAIAAAVGLGVE-PGSEVLL 114
QY 116 YRAGVGLPAARSVA-EHLSQ-GVPYKLSADDDVFLTAGTQALEVIVPVLQAOTAGANILL 173

Db 115 IEPFYDSYSPVAMAGAHRYTVPLVDPGRGFDALDALARAVTPTRTRALIINSPHPTGA 174
QY 174 PRGYPNYEARAFNKLEVRHFDLIPD-KGWEIDISLESIAKNTTAMVIINPNPCGS 232

Db 175 VLSATELAIAETAAANLVITDEVYEHVFDHARHPLAGFDGMAERTITISSAAKMF 234
QY 233 VYSYDHLAKVAEVARKLGIIVIADEVYKLVLSGSAFIPMGVFGHIA-PVLSIGSLSKSW 291

Db 235 NCTGMKIGW-A-CGPAELIAGVRAAKQYLSYVGGAPFQPA 272
QY 292 IVPGRWLGWAVYDTPKILEKTKISTITNLYNVST-DFA 330

RESULT 13
ENTRY #type complete
TITLE aspartate transaminase (EC 2.6.1.1) - Bacillus sp. (strain YM-2)
ALTERNATE_NAMES aspartate aminotransferase
ORGANISM #formal_name Bacillus sp.
DATE 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change
ACCESSION A38621
REFERENCE A38621
#authors Sung, M.H.; Tanizawa, K.; Tanaka, H.; Kuramitsu, S.; Kogamiyama, H.; Hirotsu, K.; Okamoto, A.; Higuchi, T.; Soda, K.
#journal J. Biol. Chem. (1991) 266:2567-2572
#title Thermostable aspartate aminotransferase from a thermophilic Bacillus species. Gene cloning, sequence determination, and preliminary X-ray characterization.
#cross-references MUID:91115885
#accession A38621
#status preliminary
#molecule_type DNA
#residues 1-392 ##label SUN
#cross-references GB:M59430; NID:g142537; PID:g142538
CLASSIFICATION #superfamily aspartate transaminase
KEYWORDS aminotransferase
SUMMARY #length 392 #molecular-weight 42661 #checksum 7039

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Best Local Similarity 23.5%; Pred. No. 1.71e-40;
Matches 85; Conservative 105; Mismatches 154; Indels 18; Gaps 17;

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QY 92 PAFRTAVEAEDAAALRTGQFCYAGVGLPAARSAVAEHLISQGVYKLSADDDVELTAG 151

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Db 159 KNAITDK-TKAVIINSPNPTGMVYTRREEDIAKIALENLIVDSIYEKLNGAEH 217
QY 211 -ESIADKNTTAMVIINPNPCGSYVSHDLAKVAEARKLILVIADEVYKLV-LSAP 268

Db 218 FSIQAISEVKAQIVINGVSKSHMTGWRIGYAG-NADIINAMTDLASHSTNPPTAS 276
QY 269 FIPMGVFGHI-APVLSIGSLSKSWIVPGRLGWAVYDPTKILEKTKISTITNLYNVST 327

Db 277 QYAA-I-EAY-NGPQDSVEEMRKAFESRL-ET--I-YPKLSAIFGKVV-KPOGAFYLLP 328
QY 328 DPATFVQALPKILENTKADFRRKIIGLLKESSEICYREIKENKIYTCPHKPGSMFYV 387
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Db 329 DYSEAAQKGFASVDFEAFALLTEANVAVIPGSGFAPSTIRISVATSNLIEAERID 388
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Db 389 RF 390
QY 447 SF 448

RESULT 14
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ORGANISM #formal_name Pyrococcus horikoshii
DATE 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
14-Aug-1998
ACCESSIONS
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probable aspartate aminotransferase - Pyrococcus horikoshii
#formal_name Pyrococcus horikoshii
14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
14-Aug-1998
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Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.;
Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.;
Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.;
Nakazawa, H.; Takamiya, M.; Ohfuku, Y.; Funahashi, T.;
Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kishida, N.; Oguchi,
A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.
DNA Res. (1998) 5:55-76
Complete sequence and gene organization of the genome of a
hyper-thermophilic archaeobacterium, Pyrococcus horikoshii
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#cross-references MUID:98344137
#accession E71125
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#note this accession replaces an interim accession for a
sequence replaced by GenBank
GENETICS
#gene PH0771
SUMMARY
#length 391 #molecular-weight 44565 #checksum 193
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Best Local Similarity 28.4%; Pred. No. 1.50e-35;
Matches 103; Conservative 82; Mismatches 148; Indels 30; Gaps 29;

Db 42 PDFTPKNIKAARALDEG-WHYHTNAGIPELREAVVEYKKFYGIDIEVENVIITAG 100
QY 92 PAFRTAVEAEDAVAAALRTGQFNCTAAGVGLPAARSVAEHLSSQGVPKLSADDFLTAG 151
Db 101 AYEGLTAFESLLER-GDEVIIPDPFVSVAEDAQVAEK-PVR-IPLRENNFLPPNE 157
QY 152 GTQAEIVIPVLAQTAGANILLPRGPVNY-E-ARAFNKLEVEHFLLIPDKGWEIDIDS 209
Db 158 LLEKIS-KNTR-MIVINYPNNTGATLD-KELAKTIADIAEDYNIYILSDPEYHFHYED 214
QY 210 L-ESIADKNNTAMVIIN-PNNPCGSVSYSDHLAK-VAEAVARKLGIIVADEVYKLVLS 266
Db 215 AKHPYMKIKAPENTILA-NSFSKTFMTGWRGLFV-V-APSOVI-K-EM-TKLHAYV-IG 267
QY 267 APFIPMGVFGHIAFVLSIGSLGSWIPVPGWRLGWVAVYDPTKILEKTKISTISYINLVNS 326
Db 268 -NVASFVQIAGIEAL-RS-EESKAVEMKKEYNERRKIVVVKRLKNMPGIKVKEPKGAFY 324
QY 327 TDPATFVQEALPKILENTKADFFRIICLLKESSEICVREIKENYITCPH-K-PEGSME 384
Db 325 VFPNIS-G-TGMSE-KFSEWLLKARVVVPGTAFGRMGEGVVRISYATSKELTEAM 380
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QY 443 ERV 445

RESULT 15

ENTRY #type complete

TITLE #formal_name Bacillus subtilis

ORGANISM #formal_name Bacillus subtilis

DATE 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change

24-Sep-1998

ACCESSIONS

REFERENCE #authors

Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.;

Alloni, G.; Azevedo, V.; Bertero, M.G.; Bessieres, P.;

Bolotin, A.; Borchert, S.; Boriss, R.; Boursier, L.; Brans,

A.; Braun, M.; Brigneau, S.C.; Bron, S.; Brouillet, S.;

Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;

Choi, S.K.; Codani, J.J.; Connerton, I.F.; Cummings, N.J.;

Daniel, R.A.; Denizot, F.; Devine, K.M.; Duesterhoeft, A.;

Enright, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.;

Fabret, C.; Ferrarri, E.; Foulger, D.; Fritz, C.; Fujita,

M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleron, N.; Ghim,

S.Y.; Glaser, P.; Goffeau, A.; Golightly, E.J.; Grandi, G.;

Guiseppi, G.; Guy, B.J.; Haga, K.; Haiech, J.; Harwood,

C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.;

Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Karamata, D.;

Kasahara, Y.; Klaer-Blanchard, M.; Klein, C.; Kobayashi,

Kunita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.;

Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.;

Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno,

M.; Moestli, D.; Nakai, S.; Noback, M.; Noone, D.; O'Reilly,

M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro,

V.; Pohl, T.M.; Portetelle, D.; Porwollik, S.; Prescott, G.;

A.M.; Presecan, E.; Pujic, P.; Purnelle, B.; Rapoport, G.;

Rev, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.;

Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, E.;

Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.;

Sekowska, A.; Seror, S.J.; Serrot, P.; Shin, B.S.; Soldo,

B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takanashi, H.;

Takemaru, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, T.;

Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.;

Vandenbol, M.; Vannier, F.; Vassarotti, A.; Viari, A.;

Wambutt, R.; Wedler, E.; Wedler, H.; Weitzenecker, T.;

Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto,

K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumbstein, E.;

Yoshikawa, H.; Danchin, A.

Nature (1997) 390:249-256

The complete genome sequence of the Gram-positive bacterium

Bacillus subtilis.

#cross-references MUID:98044033

#accession C69591

#status preliminary; nucleic acid sequence not shown;

translation not shown

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PID:g2634655

#experimental_source strain 168

GENETICS

#gene aspb

CLASSIFICATION

SUMMARY

#superfamily aspartate transaminase

#length 393 #molecular-weight 43088 #checksum 6856

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Best Local Similarity 23.2%; Pred. No. 1.50e-35;

Matches 85; Conservative 117; Mismatches 145; Indels 20; Gaps 18;

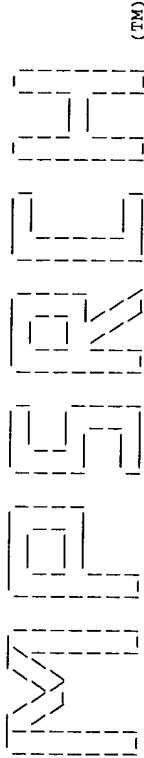
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QY 210 L-ESIADKNTTAMVIINPNPCGSVSYDHLAKVAEVARKLGIILVIADDEVYKLVLSAP 268
Db 215 HYSIAQLSDRLXEOVTIINGVSKSHSMTCWRIGYAA--GSEDII-KA-M-TNLASH-STS 268
QY 269 FIPMGVFG-HI-APVLSIGLSKSWIVPGWRIGWVAVYDPTKILEKTKISTITNYLNVS 326
Db 269 -NPTSIQYQ-AIAAYNGSPSEPLEEMREAFEHRLNTIYAKLIEIPGFSCV-KPEGAFYLF 325
QY 327 TDPATFVQEQALPKILENTKADFCKRIIGLLKESSEICYEIKENKYITCPHKPEGSMFVM 386
Db 326 PNAKEAAQSCGPKVDVEFKALLEEKVAIVPGSGFSPENVRLSYATSLDLLEAIERI 385
QY 387 VKLNHLLE-EIHDIDDFCCKLAKEESVILCFGSVLGMENWVRITFACVPSSLQDGLERV 445
Db 386 KREVEKH 392
QY 446 KSPCORN 452

Search completed: Fri Oct 1 13:52:21 1999
Job time : 28 secs.



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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Fri Oct 1 13:50:18 1999; MasPar time 15.42 Seconds
Tabular output not generated. 844.953 Million cell updates/sec

Title: >US-09-026-400-2
Description: (1-461) from US09026400.pep
Perfect Score: 3223
Sequence: 1 MVHQSNHGGEAAAAANGKS.....LERYKSFQNRKKNSINGC 461

Scoring table: PAM 150
Gap 11

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 51.018; Variance 91.346; scale 0.559

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description	Pred. No.
1	920	28.5	454	1 ATTY_RAT TYROSINE AMINOTRANSFER	3.49e-173
2	914	28.4	454	1 ATTY_HUMAN TYROSINE AMINOTRANSFER	8.32e-172
3	570	17.7	416	1 ATTY_TRYCR TYROSINE AMINOTRANSFER	5.46e-94
4	394	12.2	401	1 AAT_SULSO ASPARTATE AMINOTRANSFER	1.09e-55
5	368	11.4	375	1 AAT1_METJA PUTATIVE ASPARTATE AMI	3.41e-50
6	358	11.1	392	1 AAT_BACSP ASPARTATE AMINOTRANSFER	4.28e-48
7	345	10.7	393	1 AAT_BACST ASPARTATE AMINOTRANSFER	2.22e-45
8	330	10.2	393	1 AAT1_BACSU ASPARTATE AMINOTRANSFER	2.86e-42
9	301	9.3	392	1 PATA_BACSU PUTATIVE AMINOTRANSFER	2.51e-36
10	300	9.3	592	1 ALAM_YEAST PUTATIVE ALANINE AMINO	4.00e-36
11	294	9.1	507	1 ALAT_YEAST PUTATIVE ALANINE AMINO	6.58e-35
12	285	8.8	400	1 AATA_RHIME ASPARTATE AMINOTRANSFER	4.29e-33
13	258	8.0	444	1 YUG0_YEAST HYPOTHETICAL AMINOTRAN	1.01e-27
14	255	7.9	505	1 ALAT_SCHPO PUTATIVE ALANINE AMINO	3.91e-27
15	241	7.5	410	1 AATB_RHIME ASPARTATE AMINOTRANSFER	2.09e-24
16	243	7.5	421	1 YDT4_SCHPO HYPOTHETICAL AMINOTRAN	8.56e-25
17	235	7.3	386	1 YBOL_ECOLI HYPOTHETICAL AMINOTRAN	3.00e-23
18	231	7.2	482	1 ALA2_HORVU ALANINE AMINOTRANSFERA	1.75e-22
19	222	6.9	387	1 PATB_BACSU PUTATIVE AMINOTRANSFER	9.06e-21
20	221	6.9	399	1 AAT2_BACSU PROBABLE ASPARTATE AMI	1.40e-20
21	222	6.9	517	1 IAIC_DIACA 1-AMINOCYCLOPROPANE-1-	9.06e-20
22	217	6.7	482	1 ALA2_PANMI ALANINE AMINOTRANSFERA	7.96e-20
23	211	6.5	213	1 AAT_STRGR PROBABLE ASPARTATE AMI	1.06e-18

24	211	6.5	385	1 HIS8_YEAST HISTIDINOL-PHOSPHATE A	1.06e-18
25	210	6.5	418	1 YD91_METJA PUTATIVE AMINOTRANSFER	1.63e-18
26	207	6.4	412	1 YFD2_ECOLI HYPOTHETICAL AMINOTRAN	5.88e-18
27	199	6.2	475	1 IA12_CUCMA 1-AMINOCYCLOPROPANE-1-	1.75e-16
28	195	6.1	361	1 HIS8_HALVO HISTIDINOL-PHOSPHATE A	9.44e-16
29	195	6.1	495	1 ALAT_RAT ALANINE AMINOTRANSFERA	9.44e-16
30	187	5.8	470	1 XJIR_ECOLI HYPOTHETICAL 53.0 KD P	2.64e-14
31	185	5.7	376	1 HIS8_SULSO HISTIDINOL-PHOSPHATE A	6.02e-14
32	179	5.6	493	1 IA11_CUCMA 1-AMINOCYCLOPROPANE-1-	7.02e-13
33	177	5.5	493	1 IA11_CUCPE 1-AMINOCYCLOPROPANE-1-	1.58e-12
34	176	5.5	495	1 ALAT_HUMAN ALANINE AMINOTRANSFERA	2.37e-12
35	170	5.3	390	1 MALY_ECOLI MALY PROTEIN (EC 2.6.1	2.64e-11
36	166	5.2	494	1 IA12_CUCPE 1-AMINOCYCLOPROPANE-1-	1.29e-10
37	165	5.1	370	1 AAT2_METJA PUTATIVE ASPARTATE AMI	1.92e-10
38	164	5.1	473	1 IA1C_MALDO 1-AMINOCYCLOPROPANE-1-	2.85e-10
39	163	5.1	476	1 IA14_LYCES HISTIDINOL-PHOSPHATE A	4.22e-10
40	160	5.0	219	1 HIS8_MYCSM HISTIDINOL-PHOSPHATE A	1.36e-09
41	162	5.0	384	1 HIS8_SCHPO HISTIDINOL-PHOSPHATE A	6.24e-10
42	160	5.0	407	1 YU16_MYCTU PUTATIVE AMINOTRANSFER	1.36e-09
43	158	4.9	366	1 YB66_HAEIN PROBABLE AMINOTRANSFER	2.96e-09
44	155	4.8	359	1 HIS8_SALTY HISTIDINOL-PHOSPHATE A	9.42e-09
45	156	4.8	373	1 HIS8_METJA PROBABLE HISTIDINOL-PH	6.41e-09

ALIGNMENTS

RESULT	1	STANDARD;	PRT;	454 AA.
ID	ATTY_RAT			
AC	P04694;			
DT	13-AUG-1987 (REL. 05, CREATED)			
DT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSINE:2-OXOGLUTARATE			
DE	AMINOTRANSFERASE) (TAT).			
GN	TAT.			
OS	RATTUS NORVEGICUS (RAT).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;			
OC	RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; RATTUS.			
RP	SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE; 89079691.			
RA	HARGROVE J.L., SCOBLE H.A., MATHEWS W.R., BAUMSTARK B.R.,			
RA	BIEMANN K.;			
RA	GRANGE T., GUENET C., DIETRICH J.-B., CHASSEROT S., FROMONT M.,			
RA	BEFORT N., JAMI J., BECK G., PICTET R.;			
RT	"Complete complementary DNA of rat tyrosine aminotransferase			
RT	messenger RNA. Deduction of the primary structure of the enzyme.";			
RL	J. MOL. BIOL. 184:347-350(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE; 89079691.			
RA	HARGROVE J.L., SCOBLE H.A., MATHEWS W.R., BAUMSTARK B.R.,			
RA	BIEMANN K.;			
RA	GRANGE T., GUENET C., DIETRICH J.-B., CHASSEROT S., FROMONT M.,			
RA	BEFORT N., JAMI J., BECK G., PICTET R.;			
RT	"The structure of tyrosine aminotransferase. Evidence for domains			
RT	involved in catalysis and enzyme turnover.";			
RL	J. BIOL. CHEM. 264:45-53(1989).			
RN	[3]			
RP	SEQUENCE OF 190-386 FROM N.A.			
RC	TISSUE=LIVER;			
RX	MEDLINE; 92190544.			
RA	MOROZOV I.V.;			
RT	"Nucleotide sequence of rat liver tyrosine aminotransferase gene			
RT	fragment.";			
RL	DNA SEQ. 1:151-155(1990).			
RN	[4]			
RP	PARTIAL SEQUENCE.			
RX	MEDLINE; 92038067.			
RA	LOEBER B., DIETRICH J.-B., KERN D.;			
RT	"Isolation and characterization of active N-terminal truncated apo-			
RT	and holoenzyme of mammalian liver tyrosine aminotransferase.";			
RL	FEBS LETT. 291:345-349(1991).			
RN	[5]			
RP	STRUCTURAL PROPERTIES.			
RX	MEDLINE; 89000971.			
RA	DIETRICH J.-B., GENOT G., BECK G.;			

[illegible]

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RESULT 5
ID AATL1_METUA STANDARD; PRT; 375 AA.
AC Q60317;
DT 01-NOV-1997 (REL. 35, CREATED)
DT 01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PUTATIVE ASPARTATE AMINOTRANSFERASE 1 (EC 2.6.1.1) (TRANSAMINASE A)
DE (ASPART).
DE
DE
GN MJ0001.
OS METHANOCOCCUS JANNASCHII.
OC ARCHAEA; EURYARCHAEOTA; METHANOCOCCALES; METHANOCOCCACEAE;
OC METHANOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE; 96337999.
RA BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
RA KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
RA OVERBEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
RA SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
RA COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKIY M.,
RA KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL SCIENCE 273:1058-1073(1996).
CC -1- CATALYTIC ACTIVITY. L-ASPARTATE + 2-OXOGLUTARATE = OXALOACETATE +
CC L-GLUTAMATE (BY SIMILARITY).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
CC EMBL; U67459; G1592252; -.
CC TIGR; MJ0001; -.
CC DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
CC DR PFAM; PF00155; aminotran_1; 1.
CC KW TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
CC FT BINDING 223 223 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC SEQUENCE 375 AA; 42395 MW; 166A9EFC CRC32;
CC
CC Query Match 11.4%; Score 368; DB 1; Length 375;
CC Best Local Similarity 26.3%; Pred. No. 3.41e-50;
CC Matches 78; Conservative
CC
CC Db 33 PDBFDPKHI1EAAKRALDGKTH-YSPNNGIPELFEETISNKKDYNDLVKDNIIVTCG 91
CC QY 92 PAFRTAVAEADVAALRTGTGFNCVAGVGUPAARSVAEHLSGVPYKLSADDDVFLTAG 151
CC Db 92 AEEALMLSIMTLIDR-GDEVILPNPSFVSYLSLTETFAEGTKNIDL--DENFNIDLEKVK 148
CC

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QY	152	GTQIAEVIIPVLAQTAGANILLPRPGYPNVEARAANKLEVRHFDLIPDKGWEIDTDSL-	210
Db	149	ESIT-KTKTILIFNSPSNCTKYVDKETIKGLAEIAEDYNLIIVSEVDYDKIYDKKHS	207
QY	211	ESTADKNTTAMWIINPNPCGSVSYSDHLAKVAEVARKEILVIADEVTKLVLSAPPI	270
Db	208	PMQ-FTDRC-IL-INGESKTYAMTGWRIAGVLSDELNKELDILNNMKIKHY-SFAC-A	262
QY	271	PMGVFGHIAPVLISGLSKSWIIPVGRLGMVAYDP-TKILEKTKISTITNVLNVSTDP	329
Db	263	TTAQYGCALA-ALRGSQ-KCEDWDEFEKMRDRLLIYNGLKDI-FKV-NKPDGAYYI	314
QY	330	ATFVQ-EALPKILIENTKADFRIIIGLLKSSICRYREIKENKIYITCPHSGSFMV	385

RESULT	6	STANDARD;	PRT;	392 AA.
ID	AAT_BACSP			
AC	P23034;			
DT	01-NOV-1991 (REL. 20, CREATED)			
DT	01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPART).			
OS	BACILLUS SP. (STRAIN IM-2).			
OC	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;			
OC	BACILLUS.			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE; 91115885.			
RA	SUNG M.H., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H.,			
RA	HIROTSU K., OKAMOTO A., HIGUCHI T., SODA K.;			
RT	"Thermostable aspartate aminotransferase from a thermophilic Bacillus			
RT	species. Gene cloning, sequence determination, and preliminary X-ray			
RT	characterization."			
RL	J. BIOL. CHEM. 266:2567-2572(1991).			

[2]
SEQUENCE OF 1-24 AND 387-392.
RP MEDLINE: 90170846.
RX SUNG M.H., TANIZAWA K., TANAKA H., KURAMITSU S., KAGAMIYAMA H.,
RA SODA K.,
RT "Purification and characterization of thermostable aspartate
RT aminotransferase from a thermophilic Bacillus species."
RL J. BACTERIOL. 172:1345-1351(1990).
CC -!- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXOGLOUTARATE = OXALOACETATE +
CC L-GLUTAMATE.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -!- SUBUNIT: HOMODIMER.
CC -!- THIS THERMOSTABLE ENZYME IS MOST ACTIVE AT 70 DEGREES CELSIUS.
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.

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CC -----
DR EMBL; M59430; G142538; -
DR PIR; A38621; A38621.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR PFAM; PF00155; aminotran_1; 1.
DR TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
KW BINDING 239 239
FT CONFLICT 388 388 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ CONFLICT 388 388 D -> L (IN REF. 2).
ST SEQUENCE 392 AA; 42661 MW; 8F0EC6D0 CRC32;

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Query Match 11.1%; Score 358; DB 1; Length 392;
Best Local Similarity 23.5%; Pred. No. 4,28e-48;
Matches 85; Conservative 105; Mismatches 154; Indels 18; Gaps 17;

D_b 42 PDFTPQNTMDAAIDPSWQSG-YTKYTPSGGLPALKQAIIEKFKRDNQLEYKPNIEIVGVG 100
| | | : | | : : : | : : | | | : |

Qy	92	PAFTAVEAEDAVAAALRTGQFNCTAGAVGLPAARSVAEHL	SQGVYPKLSADDFLTAG	151
Db	101	AKHXYLTLFVILN-EGDEVILPIPYWVSPEOVKLAG-CVPYV	IEATSEQNVKIITAEOL	158
Qy	152	GTOAIEWIIPVLAQTACANILLPRPGVPNTVEARAANKLEVRHF-DLIPDKGWEIDISL	210	
Db	159	KNATDK-TRAVIINSPNPTGMVYTREELEDIAKALENNILIVSDEIVEIKLLYNAGEH	217	
Qy	211	-ESIADKNTTAMVIINPNPCGSVSYDHLAKVAEYARKLGLIVIADEVYKLVL-GSAP	268	
Db	218	FSIAQIESEVKAQTIYVINGVSKSHSTGWRIGYAAG-NADIINAMTDLASHSTSNPTTAS	276	
Qy	269	FIPMGVFGHI-APVLSIGSLSKSWIPVPGWGLGVAVVDP	TKILEKTKISTITNYLNVEST	327
Db	277	QYAA-I-EAV-NGPODSVEEMRKAFESRL-ET--I-YPKLSATPGFKVV-KQOGAFYLLP	328	
Qy	328	DPATFVQALPKILENTKADOFFRRIIGLLKESSEICYRIKENKYITCPHKPEGSMFVNV	387	
Db	329	DVSEAAQKTGFASDEFASALLTEANVAVIPGFGCAPSTIRISYATSNLTFEEATERID	388	
Qy	388	KLNHLLEEHTDDID-FCCKLAREESVILPCGVLGMENWVRITFACVPSSLDGLERVK	446	
Db	389	RF	390	
Qy	447	SF	448	

RESULT	7		
ID	AAT_BACST	STANDARD;	PRT; 393 AA.
AC	Q59228;		
DT	01-NOV-1997	(REL. 35, CREATED)	
DT	01-NOV-1997	(REL. 35, LAST SEQUENCE UPDATE)	
DT	01-NOV-1997	(REL. 35, LAST ANNOTATION UPDATE)	
DE	ASPARTATE AMINOTRANSFERASE (EC 2.6.1.1) (TRANSAMINASE A) (ASPAT).		
GN	ASPC.		
OS	BACILLUS STEAROTHERMOPHILUS.		
OC	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; BACILLACEAE;		
OC	BACILLUS.		
RN	[1]		
SEQUENCE FROM N.A.			
RP	STRAIN=ATCC 12980;		
RC	MEDLINE; 96434469.		
RX			
RA	BARTSCH K., SCHNEIDER R., SCHULZ A.;		
RT	"Stereospecific production of the herbicide phosphinothricin		
RT	(glufosinate): purification of aspartate transaminase from Bacillus		
RT	stearothermophilus, cloning of the corresponding gene, aspC, and		
RT	application in a coupled transaminase process." ;		
RL	APPL. ENVIRON. MICROBIOL. 62:3794-3799(1996).		
CC	-1- CATALYTIC ACTIVITY: L-ASPARTATE + 2-OXYGLUTARATE - OXALOACETATE +		
CC	L-GLUTAMATE.		
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE.		
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT		
CC	AMINOTRANSFERASES.		

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CC -----
DR EMBL: X93600; E212847; -.
DR PROSITE: PS00105; AA.TRANSFER_CLASS_1; 1.
DR PFAM: PF00155; aminotran_1; 1.
DR TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
KW BINDING 237 237 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT BINDING 237 237 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 393 AA; 42401 MW; 649AD162 CRC32;

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Query Match 10.7%; Score 345; DB 1; Length 393;
Best Local Similarity 23.8%; Pred. No. 2.22e-45;
Matches 86; Conservative 104; Mismatches 154; Indels


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-----
DR EMBL; U53880; G1256891; -
DR EMBL; Z73261; E245543; --
KW HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;
KW PYRIDOXAL PHOSPHATE; MITOCHONDRION; TRANSIT PEPTIDE.
FT TRANSIT 1 ? 592 MITOCHONDRION (POTENTIAL).
FT CHAIN ? 592 PUTATIVE ALANINE AMINOTRANSFERASE,
FT MITOCHONDRIAL.
FT BINDING 412 412 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 592 AA; 66421 MW; 5769BA88 CRC32;
Query Match 9.3%; Score 300; DB 1; Length 592;
Best Local Similarity 32.9%; Pred. No. 4.00e-36;
Matches 54; Conservative 50; Mismatches 53; Indels 7; Gaps 4;
Db 221 YSSQGVGIRKSAVEFITTKRDEGISVPDIFLTAGASAANNVLLSIFCRGPETGLIP 280
   I::: L::: : : : : : : : : : : : : : : : : : : : : : : : :
QY 116 YAAGVGLPAARSVAEHLSCQPVPKLS-ADDFVTAGTQTAEIVIIPVLQAQTGANILLP 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 281 IPQVPLVTATLALNNSQALPYLDENSGWSTNPPEIEITVVKEAIONEIKPTLVVINPGN 340
   I::: L::: : : : : : : : : : : : : : : : : : : : : : : :
QY 175 RPYGVNEYEARAAFNKLVRHFDLPDKGWEL---DIDSL--ESI-ADKNMTAMVIINPN 228
   I::: L::: : : : : : : : : : : : : : : : : : : : : : : :
Db 341 PTGAVLSPESIAQIFEAAKYGTGVWIADEVYQENIFFPGTKFHSM 384
   I::: L::: : : : : : : : : : : : : : : : : : : : : : : :
QY 229 PCGSVSYDIHLAKVAEVARKLGILVIADEVYKGVLVGSAFFIPM 272
   I::: L::: : : : : : : : : : : : : : : : : : : : : : : :
RESULT 11
ID ALAT YEAST STANDARD; PRT; 507 AA.
AC P52892;
DT 01-OCT-1996 (REL. 34, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE PUTATIVE ALANINE AMINOTRANSFERASE (EC 2.6.1.2) (GLUTAMIC--PYRUVIC
DE TRANSAMINASE) (GPT) (GLUTAMIC--ALANINE TRANSAMINASE).
GN YDR11C OR YD9727.07C
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
OC SACCHAROMYCETACEAE; SACCHAROMYCES.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=5288C / AB972;
RA MURPHY L., SHORE L., HARRIS D., BARRELL B.G., RAJANDREAM M.A.,
RA WALSH S.V.;
RL SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
CC -|- CATALYTIC ACTIVITY: L-ALANINE + 2-OXOGLOUTARATE = PYRUVATE +
CC L-GLUTAMATE.
CC -|- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -|- SIMILARITY: TO OTHER SPECIES ALANINE AMINOTRANSFERASE.
-----
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CC or send an email to license@isb-sib.ch).
-----
DR EMBL; Z48758; G747886; -.
KW HYPOTHETICAL PROTEIN; TRANSFERASE; AMINOTRANSFERASE;
KW PYRIDOXAL PHOSPHATE.
FT BINDING 327 327 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 507 AA; 56769 MW; 5F791EE2 CRC32;
```

Best Local Matches	Similarity	Conservative	Mismatches	Indels	Gaps
61	54	61	77	9	6

Db	31	RDVIGLGAEPD-FDT-PDNIK-KAALDAIDR-GEUK-YTPVSYGIPELREATAKKEKREN	85
Qy	78	RPVLP ^{LAH} GDPSVFPAPRTAVEAEDAVAALRTGQNCYAAGVGLPAAKSAVAEHISQGV	137
Db	86	NLDYTAQTI ^{VG} GGQILFNFAEWATLN--PGDEVIPAPYWSYSEPMVALCG-GT ^P VFV	142
Qy	138	PYKLSADDDV ^{EL} TAGGTQAI-EVILPVLAQTAGANILLPRGYPNYEARAFNKL ^{EV} RHFD	196
Db	143	PTREQENNFKLAE ^{DL} DRAPITPKTKWFNSPNSPGAAYSHEELKALT ^{DL} VMKHPHVWL	202
Qy	197	LI-PDKGWEID ^{DS} LESIAKDNTAMVILPNPNPCGSVSYD ^{SL} AKVAEVARLKG-ILVI	254
Db	203	TDDMYEHL ^T GDGFRFATPVEVEGLVERTILTMNGSVKAYAMTGW ^{RI} CYAA-CPLH-LIK	259
Qy	255	ADEVYGLKVL ^{GS} APF-IPMGV-FGHIAPVLSISLSKSWITVQWRLGWAVYDPT ^{IL} EK	312
Db	260	A-MDM-TQG-QQTS-GAASIAQAAVEALNGPQ-DF ^T IGRNKEIFQRR ^{DL} IVWSMLNQAKG	314
Qy	313	TKISTSTNVLN ^{VS} TDPA ^T FVQ ^{AL} PKILENTKADFKRIIGLLKESSEIC ^Y EIRENKY	372
Db	315	ISCP-TPEGAFYVYPSCAGLIGKTAPSGKVIETDEDFVSELLE ^T EGVAVVHGSAFGL ^{GP} N	373
Qy	373	ITC ^{HK} PEGGSMEYMK-LNL--HLL--EE-IHDDIDPCCKLAKESVIL ^{CP} SGSVLGNW	426
Db	374	FRISATSEALLEEACRRIORFC	396
Qy	427	VRITFACVP ^{SS} LQDGLERVRK ^{SF} 449	

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RESULT 13
ID YUG0_YEAST STANDARD; PRT; 444 AA.
AC P47039;
DT 01-NOV-1995 (REL. 32, CREATED)
DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL AMINOTRANSFERASE YJL060W (EC 2.6.1.-).
YJL060W OR J1138.
OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
OC EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES; SACCHAROMYCETALES;
OC SACCHAROMYCETACEAE; SACCHAROMYCETES.
[1]
RN SEQUENCE FROM N.A.
RA FORL T.M., ALJINOVIC G.;
RL SUBMITTED (SEP-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
[2]
RN SEQUENCE OF 92-222 FROM N.A.
RC STRAIN-S288C / AB972;
RX MEDLINE; 95400292.
RA MURAKAMI Y., NAITOU M., HAGIWARA H., SHIBATA T., OZAWA M.,
RA SASANOMA S., SASANOMA M., TSUCHIYA Y., SOEDA E., YOKOYAMA K.,
RA YAMAZAKI M., TASHIRO H., EKI T.;
RT "Analysis of the nucleotide sequence of chromosome VI from
RT Saccharomyces cerevisiae.";
RL NAT. GENET. 10:261-268(1995).
CC -!- COFACITOR: PYRIDOXAL PHOSPHATE (POTENTIAL).
CC -!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
CC EMBL; Z49335; G1008205; -.
DR EMBL; D44603; G871966; -.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR PFAM; PF00155; aminotran_1; 1.

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DR PFAM; PF00155; aminotran_1; 1.

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Db      277 IVLIADEVY 285
       !:::|||||
Qy      251 ILVIADEVY 259

RESULT 15
ID AATB_RHIME STANDARD; PRT; 410 AA.
AC Q06191;
DT 01-FEB-1994 (REL. 28, CREATED)
DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE ASPARTATE AMINOTRANSFERASE B (EC 2.6.1.1) (TRANSAMINASE A) (ASPART).
GN AATB.
OS RHIZOBIUM MELILOTI.
OC BACTERIA; PROTEOBACTERIA; ALPHA SUBDIVISION; RHIZOBIACEAE GROUP;
OC RHIZOBIACEAE; SINORHIZOBIUM.
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=104A14;
RX MEDLINE; 93308098.
RA ALFANO J.R., KAHN M.L.;
RT "Isolation and characterization of a gene coding for a novel
RT aspartate aminotransferase from Rhizobium meliloti.";
RL J. BACTERIOL. 175:4186-4196(1993).
CC -|- FUNCTION: INVOLVED IN SYMBIOTIC NITROGEN FIXATION.
CC -|- CATALYTIC ACTIVITY: L-ASPARATE + 2-OXOGUTARATE = OXALOACETATE +
CC L-GLUTAMATE.
CC -|- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -|- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
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DR EMBL; L12149; G152151; -.
DR PIR; A40658; A40658.
DR PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
DR PRAM; PF00135; aminotan_1; 1.
KW TRANSFERASE; AMINOTRANSFERASE; PYRIDOXAL PHOSPHATE.
FT BINDING 249 249 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 410 AA; 44453 MW; C72D06D6 CRC32;

Query Match 7.5%; Score 241; DB 1; Length 410;
Best Local Similarity 21.0%; Pred. No. 2.09e-24;
Matches 77; Conservative 100; Mismatches 174; Indels 16; Gaps 15;

Db      51 PDFPTDHVQAASDAIHGETK-YTALDGTPELKKAIREXFQENGLAYEL--DEIVA 107
       | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy     92 PAFRTAVEADAAVALATGQFNCGYAGVGUPAARSVAEHL-SQ-GVPYKLSADDVELT 149
       | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     108 TGAQKILFNMAASLD-D-PGDEVIPYTWTSYSDIVQICEGKPTLIACDASSGFRLTAQ 165
       | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy     150 AGGTOAI-EVIIPVLAQTAGANILLPRGYENEARAFNKLEVRHFPLDPKGWEIDID 208
       | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     166 KLEAITPRTRWLLNSPSNGAAYSADYRPLDLVLKHPHWLLVDVMKEHYVDYDF 225
       || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy     209 SLESIADKNTTAMWIINPNPCGSVISYDHLAKVAEVARKLG-ILVIADEVYGLVLGSA 267
       | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     226 RFVTPEARLEPKLDRKTLVNGSKAYAMTGWRIGYAGG-PRALIKAMAVVOQSQCSPSS 284
       | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy     268 PFI-PMGV-FCHIIAPVLSIGSLKSWSIVPGRWLRGWAVYDPTKILEKTKSTSIYNLV 325
       | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     285 VSQAASVAALNGPDQLFKERTESTQRRLNVVGLNA-IEGL-DCRVPEGAFYTFSGCAG 342
       ::||: | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy     326 STDPTAQVEQALPKILENTKADFTRKIITGLLGESEICYREIKENKYITCP-HKPEGSMF 384
       | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     343 VARRVTPSG-KRIESDTCFCAYLLDSHVAVVPGSAFLSYFRISYATSEAELKEALER 401

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QY 385 VVVKLNHLLEEHDDIDECCKLAKESVILCPGSLGMENWVRITFACVPSSLQDGLER 444
Db 402 ISAACKR 408
QY 445 VKSFCOR 451

Search completed: Fri Oct 1 13:50:38 1999
Job time : 20 secs.